

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 08:28:24 ; Search time 17 Seconds
(without alignments)
1206.802 Million cell updates/sec

Title: US-09-997-514-422

Perfect score: 2067

Sequence: 1 MFCLKLLLPVLLDYSGL.....RNNLEKSGGMPKTOQAF 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168	8.1	365	1	CXAR HUMAN
2	146.5	7.1	246	1	MYPO HETFR
3	146	7.1	365	1	CXAR MOUSE
4	140.5	6.8	249	1	MYPO CHICK
5	138.5	6.7	215	1	CIB2 HUMAN
6	137	6.6	215	1	EVAL MOUSE
7	137	6.6	338	1	LAMP HUMAN
8	135	6.5	338	1	LAMP RAT
9	133	6.4	686	1	IPL2 MOUSE
10	132	6.4	248	1	MYPO HUMAN
11	131	6.3	219	1	MYPO BOVIN
12	131	6.3	248	1	MYPO MOUSE
13	130	6.3	248	1	MYPO RAT
14	128.5	6.2	319	1	A33 HUMAN
15	128	6.2	686	1	IPL2 HUMAN
16	127.5	6.2	215	1	CIB2 RAT
17	127	6.1	316	1	FCGA PANTR
18	125.5	6.1	1040	1	EG15 CAEBL
19	123.5	6.0	285	1	FCG2 RAT
20	123.5	6.0	595	1	SILL HUMAN
21	123.5	6.0	1363	1	VGR3 MOUSE
22	122.5	5.9	338	1	LAMP CHICK
23	120.5	5.8	597	1	SILL PANTR
24	119	5.8	696	1	IPL1 HUMAN
25	119	5.8	696	1	IPL1 PANTR
26	119	5.8	764	1	PIGR HUMAN
27	118.5	5.7	317	1	FCGA HUMAN
28	118.5	5.7	1298	1	VGR3 HUMAN
29	118	5.7	333	1	AWAL DROME
30	118	5.7	898	1	FAS2 SCHAM
31	117.5	5.7	215	1	EVAL HUMAN
32	116.5	5.6	513	1	SHS1 MOUSE
33	116	5.6	695	1	IPL1 MOUSE

RESULT 1

ID	CXAR HUMAN	STANDARD	PRT	365 AA
AC	P78310; O00694;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-adenovirus receptor) (hCAR) (CVB3 binding protein).			
GN	CXADR OR CAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Butheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97190109; PubMed=9036860;			
RA	Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,			
RA	Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.,			
RT	"Isolation of a common receptor for Coxsackie B viruses and			
RT	adenoviruses 2 and 5,"			
RL	Science 275:1320-1323 (1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97250541; PubMed=9096397;			
RA	Tomko R.P., Xu R., Philipson L.,			
RT	"HCR and MCAR: the human and mouse cellular receptors for subgroup C			
RT	adenoviruses and group B coxsackieviruses,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356 (1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20008750; PubMed=10543405;			
RA	Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,			
RA	Bowles N.E.;			
RT	"Genomic organization and chromosomal localization of the human			
RT	Coxsackievirus B-adenovirus receptor gene,"			
RL	Hum. Genet. 105:354-359 (1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;			
RT	"Sequence and expression of CXADR, the human gene for the			
RT	coxsackievirus and adenovirus receptor,"			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Anderson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,			
RA	Sollerbrant K., Sonhammer E., Philipson L.;			
RT	"Putative regulatory domains in the human and mouse CAR genes,"			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cervix;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			

34	116	5.6	2012	1	DSCA HUMAN	O60469 homo sapien
35	115.5	5.6	298	1	JAM1_BOVIN	Q9xt56 bos taurus
36	115.5	5.6	499	1	SIL8_HUMAN	Q9ny24 homo sapien
37	115	5.6	696	1	IPL1_RAT	P59824 rattus norv
38	113.5	5.5	4391	1	FGBM_HUMAN	P98160 homo sapien
39	112	5.4	353	1	CEPU_CHICK	Q90773 gallus gall
40	112	5.4	1493	1	NEO1_MOUSE	P21995 mus musculu
41	110.5	5.3	330	1	EMB_MOUSE	Q8hxj7 macaca fasc
42	110	5.3	215	1	CIB3_MACFA	Q9p2b2 homo sapien
43	109.5	5.3	879	1	PFRP_HUMAN	O94856 homo sapien
44	109.5	5.3	1240	1	NPAS_HUMAN	Q9ny72 homo sapien
45	109	5.3	215	1	CIB3_HUMAN	

ALIGNMENTS

Mon Mar 15 08:43:01 2004

```
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC -!- SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; Y07593; CAA68868.1; -.
CC EMBL; U90716; AAC51234.1; -.
CC EMBL; AF169366; AAF05908.1; -.
CC EMBL; AF169360; AAF05908.1; JOINED.
CC EMBL; AF169361; AAF05908.1; JOINED.
CC EMBL; AF169362; AAF05908.1; JOINED.
CC EMBL; AF169363; AAF05908.1; JOINED.
CC EMBL; AF169364; AAF05908.1; JOINED.
CC EMBL; AF169365; AAF05908.1; JOINED.
CC EMBL; AF200465; AAF24344.1; -.
CC EMBL; AF242865; AAG01088.1; -.
CC EMBL; AF242862; AAG01088.1; JOINED.
CC EMBL; AF242864; AAG01088.1; JOINED.
CC EMBL; BC003684; AAH03684.1; -.
CC EMBL; BC010536; AAH10536.1; -.
CC PDB; 1E4J; 13-JUL-01.
CC PDB; 1F5W; 08-NOV-00.
CC PDB; 1KAC; 24-NOV-99.
CC Genew; HGNC:2559; CXADR.
CC MIM; 602621; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003598; IG_C2.
CC Pfam; PF00047; IG; 2.
CC SMART; SM00408; Igc2; 1.
CC PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT DOMAIN 238 258
FT TRANSMEM 259 365
FT DOMAIN 20 134
FT DOMAIN 20 134
FT DOMAIN 141 228
FT DISULFID 41 120
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
FT SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;
Query Match 8.1%; Score 168; DB 1; Length 365;
Best Local Similarity 21.8%; Pred. No. 2e-06;
Matches 87; Conservative 65; Mismatches 148; Indels 100; Gaps 18;
QY 5 LKLLPVLVDYSLGNDLNVPPPELTVH--VGDLSALMGCVQ-STEDKCIKFDWTLSP 61
DB 5 LCFVLLCGVDFFA---RSLSIITPEEMIEKAKGETAYLPCKFTLSPEQDPLDIWLISP 61
QY 62 GEHAKDEYLYVYVNSLVPIGRF---QNRVHL-MGDILCDGSLLLQDVQVQADQGYICE 117
DB 62 AUNQKVDQVILLYSGDKIYDDYYPDLKGRVHFTSNDLKSGLASINVTNLQSLDITGYQCK 121
QY 118 IRLKGSQVFKKXAVLVHLPPEPKELMHVGGLIQMGCVF-----QSTEVKHVTKVWIFIS 173
DB 122 V--KXAPGVANKIHLWL--VKPSGARCYVDGSEETGSDFKIKCEPKESLPLQYEW--- 175
QY 174 GRRAKEIVFRYYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSLMQLQGVRESDDGNYT 233
DB 176 -----QKLSDSQKMTSW-----LAETSSV-----TSVKNASSEYSTYS 211
QY 234 CSTHLGNLVFKTIVLHVSPEEPTLVTPAALRPLVLGNQNLVIIVGIVCATILLPLVI 293
DB 212 CTVR--NRVGSQDCLRLNVVP-----SNKAGLIAGAIITGLALALIG 254
QY 294 LIYKKTGCKNKS VSNVTVLVKNYKTNPEIKKEKCHPERCEGEBKHYSFIIVREVIEEEP 353
DB 255 LII-FCC-----RKKRREKYEKEVHHD-----IREDDVP 282
QY 354 SESEATYMTMHPVWPVSLRSDRNN--SLEKKSGGMPKQTQ 391
DB 283 PPKSRTSTARSY-----IGSNHSLSGMSPSNMEGYSKTQ 317
RESULT 2
MYP0_HETFR
ID MYP0_HETFR STANDARD; PRT; 246 AA.
AC P20938;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral
DE protein) (MPP).
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
OC Heterodontidae; Heterodontus.
NCBI_TaxID=7792;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90040744; PubMed=2478717;
RA Saavedra R.A., Fors L., Aebersold R.H., Arden B., Horvath S.,
RA Sanders J., Hood L.;
RT "The myelin proteins of the shark brain are similar to the myelin
RT proteins of the mammalian peripheral nervous system.";
RL J. Mol. Evol. 29:149-156(1989).
CC -!- FUNCTION: Creation of an extracellular membrane face which guides
CC the wrapping process and ultimately compacts adjacent lamellae.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system
CC Schwann cells.
CC -!- PTM: N-GLYCAN IS SULFATED (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Belongs to the myelin P0 protein family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X16714; CAB37865.1; -.

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DR PIR; A32999; A32999.
DR HSSP; P06907; INED.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR000920; Myelin_P0.
DR PRINTS; PR00213; MYELINP0.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00568; MYELIN P0; 1.
KW Myelin; Structural protein; Glycoprotein; Transmembrane;
KW phosphorylation; Immunoglobulin domain; Signal.
FT SIGNAL 1 27
FT CHAIN 28 246
FT DOMAIN 28 150
FT TRANSMEM 151 178
FT DOMAIN 179 246
FT DOMAIN 28 143
FT DISULFID 48 125
FT CARBOHYD 120 120
SQ SEQUENCE 246 AA; 27335 MW; A776A9ED9D430FA0 CRC64;

      Query Match      7.1%; Score 146.5; DB 1; Length 246;
      Best Local Similarity 26.0%; Pred. No. 7e-05;
      Matches 44; Conservative 37; Mismatches 61; Indels 27; Gaps 6;

QY 147 VGGLIQMGCVFQSTE-VKHHVTKVEMITSGRRAKEEI-VFYYHKLRMSVEYSQSGHQPQ 204
DB 40 VGS DVTLYCGFWSNEYSVDLTTLTSRRPRPDNSRDIISIFHYGN---GVFYIEKWGGFRG 95

QY 205 RVNLVIGDIFRNDGSIIMLGQVRES DGNVTCSIHLGNLVFKKTVLHVSPREPRLVTPAA 264
DB 96 RVEWVGDISKHDGSIIVRNLDYIDNGFTCDVKNPDPVGVGTSSDVHLIVVD-----K 147

QY 265 LRPLVLGGNQLVIIVGIVCATILLPLVL-----IVKKTGKNKSS 305
DB 148 IPPVGAG-----VSGAIGFTGLIILLVGGLYLFRYIVRRRARSETS 191

RESULT 3
CXAR MOUSE
ID_CXAR_MOUSE STANDARD; PRT; 365 AA.
AC P97792; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cxsackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR. (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=97190109; PubMed=9036860;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Cocksackie B viruses and
RT adenoviruses 2 and 5.";
RL Science 275:1320-1323(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RX MEDLINE=97250541; PubMed=9096197;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and mCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B cxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=98080429; PubMed=9420240;

```

Db 283 PPKSRTSTARS-IGSNHSLGSMSPSNEGYSKTQ 317

RESULT 4

MYPO_CHICK STANDARD; PRT; 249 AA.

AC P37301; 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90204597; PubMed=1690817;

RA Barbu M.;

RT "Molecular cloning of cDNAs that encode the chicken P0 protein: evidence for early expression in avians.";

RL J. Neurosci. Res. 25:143-151(1990).

CC -!- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Found only in peripheral nervous system Schwann cells.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Belongs to the myelin P0 protein family.

DR PIR; A61087; A61087.

DR HSSP; P06907; INEU.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig V.

DR InterPro; IPR000920; Myelin_P0.

DR Pfam; PF00047; Ig; 1.

DR PRINTS; PR00213; MYELINP0.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 1.

DR PROSITE; PS00568; MYELIN P0; 1.

KW Myelin; Structural protein; Glycoprotein; Transmembrane; Phosphorylation; Immunoglobulin domain; Signal.

FT SIGNAL 1 29 BY SIMILARITY.

FT CHAIN 30 249 MYELIN P0 PROTEIN.

FT DOMAIN 30 153 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 154 179 POTENTIAL.

FT DOMAIN 180 249 CYTOPLASMIC.

FT DOMAIN 20 143 IG-LIKE V-TYPE.

FT DOMAIN 50 127 POTENTIAL.

FT CARBOHYD 122 122 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 249 AA; 27466 MW; FBD14801FFBA08FB CRC64;

Query Match 6.8%; Score 140.5; DB 1; Length 249;

Best Local Similarity 26.8%; Pred No. 0.00022;

Matches 45; Conservative 34; Mismatches 70; Indels 19; Gaps 7;

QY 131 VVHLVPEEPKELMVHVGGLIQMGCVFQSTE-VKHTVKVEWIFSGRAKEEIVFYHKL 189

DB 28 LAIHVY--TPREVYGVGVSHVTLSCSFWSSEWISEDISTHFWAEGSRDSISIFHYGK- 84

QY 190 RMSVEYSQSGHFQNRVNI VGDIFRNDGSGIMLGQVRESGGNYTCSI-HLGNLVFKKT-I 247

DB 85 --GQPYIDVDGSKFERMEWGNPRKDGSIIVHNDYTDNGTFCVKNRPDPVIGKSSQV 142

QY 248 VLHVSPEEPTLVTPAALRPLVLGNQLVIVGIVCATILLPLVILI 295

DB 143 TLVLEKVTTRY-----GVVLGS-----IIGVILLVALLVAVVLYV 179

RESULT 5

CIB2_HUMAN STANDARD; PRT; 215 AA.

ID CIB2_HUMAN

AC 060939; 075302; Q9UNN3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Sodium channel beta-2 subunit precursor.

DE SCN2B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97439560; PubMed=9295116;

RA Eubanks J.; Srinivasan J.; Dinulos M.B.; Distèche C.M.; Catterall W.A.;

RT "Structure and chromosomal localization of the beta2 subunit of the human brain sodium channel.";

RL NeuroReport 8:2775-2779(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99104330; PubMed=9887383;

RA Bolino A.; Seri M.; Caroli F.; Eubanks J.; Srinivasan J.; Mandich P.; Schenone A.; Quattrone A.; Romeo G.; Catterall W.A.; Devoto M.;

RT "Exclusion of the SCN2B gene as candidate for CMT4B.";

RL Eur. J. Hum. Genet. 6:629-634(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA Isom L.L.; Mattei L.N.; Ragsdale D.S.;

RT "Primary structure and functional expression of a beta 2 subunit of human infant brain sodium channels.";

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Cruz J.S.; Santana L.F.; Frederick C.A.; Isom L.L.; Malhotra J.D.; Mattei L.N.; Kass R.S.; Xia J.; An R.-H.; Lederer W.J.;

RT "Whether 'slip-mode conductance' occurs.";

RL Science 284:711-711(1999).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.; Schuster R.D.; Collins P.S.; Wagner L.; Shenmen C.M.; Schuler G.D.; Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.; Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.; Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.; Brownstein M.J.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.; Stapleton M.; Udén T.B.; Toshiyuki S.; Carninci P.; Prange C.; Raha S.A.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.; Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.; Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.; Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.; Fahey J.; Hellon E.; Kettner M.; Madan A.; Rodriguez S.; Sanchez A.; Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.; Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.; Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.; Krzywicki M.I.; Skalska U.; Smal M.A.; Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Crucial in the assembly, expression, and functional modulation of the heterotrimeric complex of the sodium channel. The beta-2 subunit causes an increase in the plasma membrane surface area and in its folding into microvilli (By similarity).

CC -!- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-FORMING ALPHA SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY DISULFIDE BONDS (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

[illegible]

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DR EMBL; U34554; AAA86120.1; -;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor;
KW Repeat; Signal; Lipoprotein.
FT SIGNAL 1 28
FT CHAIN 29 315
FT LIMBIC SYSTEM-ASSOCIATED MEMBRANE
FT PROTEIN.
FT PROPEP 316 338
FT DOMAIN 29 122
FT DOMAIN 132 214
FT DOMAIN 219 304
FT DISULFID 53 111
FT DISULFID 153 197
FT DISULFID 239 290
FT CARBOHYD 40 40
FT CARBOHYD 66 66
FT CARBOHYD 136 136
FT CARBOHYD 148 148
FT CARBOHYD 279 279
FT CARBOHYD 287 287
FT CARBOHYD 300 300
FT CARBOHYD 315 315
FT LIPID 315 315
SQ SEQUENCE 338 AA; 37324 MW; 0876AFDD68A39B86 CRC64;
Query Match 6.5%; Score 135; DB 1; Length 338;
Best Local Similarity 19.8%; Pred. No. 0.00095;
Matches 71; Conservative 55; Mismatches 123; Indels 110; Gaps 14;
QY 4 PLKILLPLVLDVSLGN--DLNVSPPELVTHVGSALMGCVFQSTBDK-----CIF 53
Db 13 PLVLLRLCLLPTGLPVRSDVFNKGTNTVROQDGTAILRCWVEDKNSKVWLNRSGLIF 72
QY 54 --KIDWTLSPGEHAKDYLVIYYSNLSPVIGRQFQNVHLMGDILCNDGSLLLQDVQADQ 111
Db 73 AGHDKWSLDPRVLEKXHALEY-----SLRIQKVDVYDE 106
QY 112 GTYICIRLKGESQVFKKAVLVHLVLP--EPKELMVHVGLGLQMGCVFQSTEV-----K 163
Db 107 GSYTCSVQTOHEPKTSQVYLIVQVPPKISNISSDVTNVEGSLVLCMANGREPVTWIR 166
QY 164 HVTKEVWIFSGR-----RAKEEIVFYHYKLRMSVEY-----SQS 198
Db 167 HLTPGLREFEGEEYLEILGITREQSKYKCAANEVSSADVQKVYVNVYPTITESKS 226
QY 199 -----WGHFQNRVNLVG--DIFRNDG--SIMLQVRSDDGG 230
Db 227 NEATTGROASLKCEASAVPAPDEWTRDTRINSANGLEIKSTEGQSSLTVTNVTTEHYG 286
QY 231 NYTCSIHGLNVLFKKTVILHVSPEEPRTLVTPAALRPLVGLGNQVLIVGIVCATILL 289
Db 287 NYTC-----VAANKLGVTNAS-----LVLFPRQSVRG-INGSSISLAVPLWLLAASLFLCL 334
RESULT 9
IPL2_MOUSE
ID IPL2_MOUSE
AC Q9ERS6; Q9ERS6; PRT; 686 AA.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE X-linked interleukin-1 receptor accessory protein-like 2 precursor
DE (ILIRAPL-2 related protein) (TIGIR-1).
GN ILIRAPL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Brain, and Liver;
RX MEDLINE=20459050; PubMed=10882729;
RA Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S.,
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
RT of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
RX TISSUE=Brain;
RX MEDLINE=21472256; PubMed=11587848;
RA Ferrante M.I., Ghiani M., Bulfone A., Franco B.;
RA "ILIRAPL2 maps to Xq22 and is specifically expressed in the central
RA nervous system";
RT Gene 275:217-221(2001).
RL -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9ERS6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9ERS6-2; Sequence=VSP_008056, VSP_008057;
CC Note=may be due to an intron retention; -;
CC -1- TISSUE SPECIFICITY: Detected in fetal brain after day 12.5, in
CC particular in parts of the diencephalon and in the basal plate of
CC the spinal cord. In postnatal brain detected in cerebral cortex,
CC olfactory bulb, in the CAI region of the hippocampus and in
CC Purkinje cells of the Xth cerebellar lobule.
CC -1- SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
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DR EMBL; AF284437; AAG21371.1; -;
DR EMBL; AJ277831; CAC10559.1; -;
DR MGD; MGI:1913106; Ilirap12.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR004077; IL1_receptor1p.
DR Pfam; PF00047; ig; 3.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR01539; INTRLEUKNIR2.
DR PRINTS; PR01537; INTRLEUKNIRP.
DR SMART; SM00409; IG; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS50104; TIR; 1.
KW Receptor; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 686
FT X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY
FT PROTEIN-LIKE 2.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT DOMAIN 17 354
FT TRANSMEM 355 375

FT	DOMAIN	376	686	CYTOPLASMIC (POTENTIAL).
FT	FT	32	132	IG-LIKE C2-TYPE 1.
FT	DOMAIN	141	232	IG-LIKE C2-TYPE 2.
FT	DOMAIN	239	347	IG-LIKE C2-TYPE 3.
FT	DOMAIN	400	559	TIR.
FT	DISULFID	53	116	POTENTIAL.
FT	DISULFID	162	214	POTENTIAL.
FT	DISULFID	265	331	POTENTIAL.
FT	CARBOHYD	63	63	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	120	120	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	328	328	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	350	354	DLIYK -> GLIFS (in isoform 2).
FT	VARSPLIC	355	686	/FTid=VSP_008056.
FT	VARSPLIC			Missing (in isoform 2).
FT	VARSPLIC			/FTid=VSP_008057.
FT	SEQUENCE	686 AA;	78797 MW;	36160D1CDE9B8264 CRC64;
FT	SEQUENCE			6.4%; Score 133; DB 1; Length 686;
FT	SEQUENCE			Best Local Similarity 20.4%; Pred. No. 0.0035;
FT	SEQUENCE			Matches 78; Conservative 60; Mismatches 130; Indels 114; Gaps 18;
Qy	38	ALMCCVQSTEDKCFK	-----IDWTLT-----PGEHAKDEYVLVY-----YS-- 75	
Db	8	ALVVCASVSTNLKMWKRNKNSVDGCLDSVDLKTNALAGEPVVKCALFYIYRTNSMA	67	
Qy	76	NLSVPIGRFQNRVHLMGDILCN-----DGSLLQDVQADQGTTCIRLKGESQVF	127	
Db	68	QSTGLRLMWYKNGDLPEPIFSEVRMSKEEDATWFSABQDSGFYTCVLR--NSTYCM	125	
Qy	128	KKAVLVHLPBEPKELMHVHGLIQMGCVFOS-----TEVKVTKVEMI-----FSGR	176	
Db	126	KVMSLTAENE-----SLCYNSRIRYLEKSEVTRKEISCPDMDDFKSD	172	
Qy	177	AKELIVFYHKLMSVEYSQSQGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCGI	236	
Db	173	QEPDVVVVYKCKPKM-----WRSI-----ILQGNALLIQVQEDGGNYTCGL	216	
Qy	237	HLGNLVFKKTIHLVHSPPEPRTLVTPAALRPLVLGGNQLVIT-----VGIVCATILL	289	
Db	217	KVEGLVRRTELKVT-----ALLTDKPKPLFPMENQPSVIDVQLGKPLNTPCKAFPGF	271	
Qy	290	-----PVL-----ILIVKTCGNKSSVNSVLVKNVTKNTPEIKE	324	
Db	272	SGESGPMYWMKEKFIHELACHIREGEIRLLKHEHLGK-EVELTLIFDSV--VEADLAN	328	
Qy	325	KPCFPERCEGEKHYSPIIVRE	346	
Db	329	YTCHEVNRNGRKH--ASVLLRK	348	

RL	Biochem. Biophys. Res. Commun.	180:515-518 (1991).
RL	[2]	
RP	SEQUENCE FROM N.A., AND VARIANT CMT1B HIS-98.	
RC	TISSUE=Spinal cord;	
RX	MEDLINE=93356807; PubMed=7688964;	
RA	Hayasaka K., Ohnishi A., Takada G., Fukushima Y., Murai Y.;	
RT	"Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy	
RT	type 1.";	
RL	Biochem. Biophys. Res. Commun.	194:1317-1322 (1993).
RL	[3]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=94154677; PubMed=7503228;	
RX	Pham-Dinh D., Fourbil Y., Blanquet F., Mattei M.-C., Roessel N.,	
RP	Latour P., Chazot G., Vandenbergh A., Dautigny A.;	
RA	"The major peripheral myelin protein zero gene: structure and	
RT	localization in the cluster of P0 gamma receptor genes on human	
RT	chromosome 1q21.3-q23.";	
RL	Hum. Mol. Genet.	2:2051-2054 (1993).
RL	[4]	
RP	SEQUENCE FROM N.A.	
RA	Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,	
RA	Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,	
RA	Phelan M., Farmer A.;	
RT	"Cloning of human full-length CDSs in BD Creator(TM) system donor	
RT	vector.";	
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.	
RL	[5]	
RP	SEQUENCE FROM N.A.	
RP	TISSUE=Skin;	
RX	MEDLINE=22388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A.	99:16899-16903 (2002).
RL	[6]	
RP	SEQUENCE OF 24-248 FROM N.A.	
RA	Nelis E., Timmerman V., De Jonghe P., Maylle L., Martin J.-J.,	
RA	Van Broeckhoven C.;	
RT	"Linkage and mutation analysis in an extended family with Charcot-	
RT	Marie-Tooth disease type 1B.";	
RL	Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.	
RL	[7]	
RP	REVIEW ON CMT1B VARIANTS.	
RX	MEDLINE=95282670; PubMed=7762451;	
RA	Roa B.B., Lupski J.R.;	
RT	"Molecular Genetics of Charcot-Marie-Tooth neuropathy.";	
RL	Adv. Hum. Genet.	22:117-152 (1994).
RL	[8]	
RP	REVIEW ON CMT1B VARIANTS.	
RX	MEDLINE=94302675; PubMed=7518101;	
RA	Patel P.I., Lupski J.R.;	
RT	"Charcot-Marie-Tooth disease: a new paradigm for the mechanism of	
RT	inherited disease.";	
RL	Trends Genet.	10:128-133 (1994).
RL	[9]	
RP	REVIEW ON CMT1B AND DSS VARIANTS.	
RX	MEDLINE=99103460; PubMed=9888385;	

RA Nelis E., Haïtes N., van Broeckhoven C.;
RT "Mutations in the peripheral myelin genes and associated genes in
RL inherited peripheral neuropathies."; Hum. Mutat. 13:11-28(1999).
RN [10]
RP VARIANT CMT1B MET-30.
RX MEDLINE=94061030; PubMed=7694726;
RA Hayaasaka K., Takada G., Ionasescu V.V.;
RT "Mutation of the myelin P0 gene in Charcot-Marie-Tooth neuropathy
RL type 1B."; Hum. Mol. Genet. 2:1369-1372(1993).
RN [11]
RP VARIANT CMT1B CYS-82.
RX MEDLINE=94083941; PubMed=7505151;
RA Himoro M., Yoshikawa H., Matsui T., Mitsui Y., Takahashi M.,
RA Kaido M., Nishimura T., Sawaihi Y., Takada G., Hayaasaka K.;
RT "New mutation of the myelin P0 gene in a pedigree of
RL Charcot-Marie-Tooth neuropathy 1B."; Biochem. Mol. Biol. Int. 31:169-173(1993).
RN [12]
RP VARIANT CMT1B GLU-90 AND GLU-96.
RX MEDLINE=94035113; PubMed=7693129;
RA Hayaasaka K., Himoro M., Sato W., Takada G., Uyemura K., Shimizu N.,
RA Bird T.D., Conneally P.M., Chance P.F.;
RT "Charcot-Marie-Tooth neuropathy type 1B is associated with mutations
RL of the myelin P0 gene."; Nat. Genet. 5:31-34(1993).
RN [13]
RP VARIANT CMT1B SER-63 DEL.
RX MEDLINE=94035114; PubMed=7693130;
RA Kulkens T., Bollhuis P.A., Wolterman R.A., Kemp S., Te Nijenhuis S.,
RA Valentijn L.J., Hensels G.W., Jennkens F.G., de Visser M.,
RA Hoogendijk J.E., Baas F.;
RT "Deletion of the serine 34 codon from the major peripheral myelin
RL protein P0 gene in Charcot-Marie-Tooth disease type 1B."; Nat. Genet. 5:35-39(1993).
RN [14]
RP VARIANT CMT1B GLU-96.
RX MEDLINE=94068501; PubMed=7504284;
RA Su Y., Brooks D.G., Li L., Lepercq J., Trofatter J.A., Ravetch J.V.,
RA Lebo R.V.;
RT "Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B
RL patients."; Proc. Natl. Acad. Sci. U.S.A. 90:10856-10860(1993).
RN [15]
RP VARIANTS DSS CYS-63 AND ARG-167.
RX MEDLINE=94100981; PubMed=7506095;
RA Hayaasaka K., Himoro M., Sawashiki Y., Nanao K., Takahashi T.,
RA Takada G., Nicholson G.A., Ouvrier R.A., Tachi N.;
RT "De novo mutation of the myelin P0 gene in Dejerine-Sottas disease
RL (hereditary motor and sensory neuropathy type III)."; Nat. Genet. 5:266-268(1993).
RN [16]
RP VARIANTS CMT1B LEU-78 AND ASN-134.
RX MEDLINE=95080774; PubMed=7527371;
RA Nelis E., Timmerman V., de Jonghe P., Vandenberghe A., Pham-Dinh D.,
RA Dautigny A., Martin J.-J., van Broeckhoven C.;
RT "Rapid screening of myelin genes in CMT1 patients by SSCP analysis:
RL identification of new mutations and polymorphisms in the P0 gene."; Hum. Genet. 94:653-657(1994).
RN [17]
RP VARIANT CMT1B PHE-63.
RX MEDLINE=96432254; PubMed=8835320;
RA Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P.,
RA Bonnebouche C., Corbillion E., Chazot G., Vandenberghe A.;
RT "Charcot-Marie-Tooth type 1B neuropathy: third mutation of serine 63
RL codon in the major peripheral myelin glycoprotein P0 gene."; Clin. Genet. 48:281-283(1995).
RN [18]
RP VARIANTS CMT1B LEU-78 AND CYS-101.
RX MEDLINE=96055517; PubMed=7550231;
RA Latour P., Blanquet P., Nelis E., Bonnebouche C., Chapon F.,
RA Diraison P., Ollagnon E., Dautigny A., Pham-Dinh D., Chazot G.,

RA Boucherat M., van Broeckhoven G., Vandenbergh A.;
RT "Mutations in the myelin protein zero gene associated with
RT Charcot-Marie-Tooth disease type IB.";
RL Hum. Mutat. 6:50-54(1995). [19]
RX VARIANT DSS PHE-64 DEL.
RX MEDLINE=96212920; PubMed=8630052;
RA Ikedami T., Nicholson G.A., Ikeda H., Ishida A., Johnston H., Wise G.,
RA Ouvrier R.A., Hayasaka K.;
RA "A novel homozygous mutation of the myelin Po gene producing
RT Dejerine-Sottas disease (hereditary motor and sensory neuropathy
RT type III).";
RL Biochem. Biophys. Res. Commun. 222:107-110(1996). [20]
RX VARIANTS CMT1B THR-135 AND SER-137.
RX MEDLINE=96263736; PubMed=8664899;
RA Roa B.B., Warner L.E., Garcia C.A., Russo D., Lovelace R.,
RA Chance P.F., Lupeki J.R.;
RT "Myelin protein zero (MPZ) gene mutations in nonduplication type 1
RT Charcot-Marie-Tooth disease";
RL Hum. Mutat. 7:36-45(1996). [21]
RX VARIANT CMT1B SER-122.
RX MEDLINE=97001227; PubMed=8844219;
RA Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P.,
RA Bonnebouche C., Diraison P., Chapon F., Chazot G., Vandenbergh A.;
RT "Charcot-Marie-Tooth type 1B neuropathy: a mutation at the single
RT glycosylation site in the major peripheral myelin glycoprotein Po.";
RL Hum. Mutat. 8:185-186(1996). [22]
RX VARIANTS CMT1B/DSS ILE-34; CYS-98; HIS-98; ARG-130 AND LEU-135.
RX MEDLINE=96390490; PubMed=8797476;
RA Gabriels-Festen A.A.W.M., Hoogendijk J.E., Meijerink P.H.,
RA Gabriels F.J.M., Bolhuis P.A., van Beersum S., Kuikens T., Melis E.,
RA Jennekens F.G., de Visser M., van Engelen B.G., van Broeckhoven C.,

Query Match 6.4%; Score 132; DB 1; Length 248;
Best Local Similarity 26.2%; Pred. No. 0.0011;
Matches 45; Conservative 31; Mismatches 74; Indels 22; Gaps 6

Qy 129 KAVLVHLVPEPKELMVHVGGLIQMGCVFQSTE-VKHVTKVWFSGPRAKEIVFRYYH 187
Db :::|||: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
28 QAIUVYIT---DREHGAVGSRVILHCFSWSEWSDISTWRYPQEGGRDAISIFHYA 83
Qy 188 KLMSVEYTSOSGHGFQRNVNLVGDIFRNDGSIMLQGVRSDGNVTCIHLGNLIVFKKT- 246
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
84 K--GGPYIDEVGTFFKERIQWGVDPKWKGSIVIHNLDSNGFTCDVKNPDPDVGKTS 140
Qy 247 -IVLHVSPPEPRTLVTPAALRPVLGQNLVIIVGIVCATILLPLVLIIYK 297
Db :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
141 QVTLXVFEPKPTFY-----GVVLGA-----VIGGVLGVVLLLLLFYVVR 180

RESULT 11
MYPO BOVIN STANDARD; PRT; 219 AA.

ID MYPO_BOVIN ID AC PI0522;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1989 (Rel. 11, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein (Myelin protein zero) (Myelin peripheral protein)
DN (MPP).
GE MPZ.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;

RESULT	11
MYPO_BOVI	
ID_MYPO	
AC	P105
DT	01-J
DT	01-J
DT	10-O
DE	Myel
DE	(MPP
GN	MPZ
OS	Bos
OC	Euka
OC	Mamm
OC	Bovl
OX	NCBI
RN	[1]
RP	SEQU
RC	TISS
RX	MEDL
RA	Sak

Genomics 9:751-757(1991).
-!- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Found only in peripheral nervous system Schwann cells.
-!- PTM: N-LINKED GLYCAN IS SULFATED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin P0 protein family.
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EMBL; M62860; AAA39867.1; -.
EMBL; M62857; AAA39867.1; JOINED.
EMBL; M62858; AAA39867.1; JOINED.
EMBL; M62859; AAA39867.1; JOINED.
HSSP; P06907; INEU.
MGD; MGI:103177; Mpz.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
InterPro; IPR000920; Myelin_P0.
PRINTS; PR00213; MYELINP0.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG LIKE; 1.
PROSITE; PS00568; MYELIN_P0; 1.
Myelin; Structural protein; Glycoprotein; Transmembrane; Phosphorylation; Immunoglobulin domain; Signal.
FT SIGNAL 1 29 BY SIMILARITY
FT CHAIN 30 248 MYELIN P0 PROTEIN
FT DOMAIN 30 153 EXTRACELLULAR (BY SIMILARITY)
FT TRANSMEM 154 179 BY SIMILARITY
FT DOMAIN 180 248 CYTOPLASMIC (BY SIMILARITY)
FT DOMAIN 30 143 IG-LIKE V-TYPE.
FT DISULFID 50 127 POTENTIAL.
FT CARBOHYD 122 122 N-LINKED (GLCNAC...) (COMPLEX).
SQ SEQUENCE 248 AA; 27621 MW; 936D66684300C9 CRC64;
Query Match 6.3%; Score 131; DB 1; Length 248;
Best Local Similarity 25.4%; Pred. No. 0.0014;
Matches 45; Conservative 32; Mismatches 80; Indels 20; Gaps 6;
QY 124 SQVFKKAVLHVLPEEPKELMVHVGGLIQMCCVQSTF-VKHVTKVVEIFSGRRAKERIV 182
DB 21 SLVLSPLAIVVYTD--REIYGAVGSGQVTLHCFSWSEWSDDISFTWRYQPEGRDAIS 78
QY 183 FRYVHKLRMSVEYSQSGHGFQNRVNLVGDIFRNDGSIHQVRESDDGNYTCSIHLGNLV 242
DB 79 IFHYAK--GQPYIDEVGAFFKRIQWGDPRKDGSIHNLVDYSDNGTFTCDVKNPPDI 135
QY 243 FKKT--IVLHVSPEEPRTLTPAALRPLVLGNQNLVIIVGIVCATILLPVLIVK 297
DB 136 VKTQSQVTLVYFVKVTRY-----GVVLGA-----VIGGILGVLLLLLFYLIR 180
RESULT 13
MYP0_RAT
ID MYP0_RAT STANDARD; PRT; 248 AA.
AC P06507;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
DE MPZ OR P0.
GN Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

"Complete amino acid sequence of P0 protein in bovine peripheral nerve myelin";
J. Biol. Chem. 262:4208-4214(1987).
-!- FUNCTION: Creation of an extracellular membrane face which guides the wrapping process and ultimately compacts adjacent lamellae.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Found only in peripheral nervous system Schwann cells.
-!- PTM: N-LINKED GLYCAN IS SULFATED.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Belongs to the myelin P0 protein family.
PIR; A29128; A29128.
HSSP; P06907; INEU.
GlycoSuiteDB; P10522; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
InterPro; IPR000920; Myelin_P0.
PRINTS; PR00213; MYELINP0.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG LIKE; 1.
PROSITE; PS00568; MYELIN_P0; 1.
Myelin; Structural protein; Glycoprotein; Transmembrane; Phosphorylation; Immunoglobulin domain.
FT DOMAIN 1 124 EXTRACELLULAR
FT TRANSMEM 125 150
FT DOMAIN 151 219
FT DOMAIN 1 114
FT DISULFID 21 98
FT CARBOHYD 93 93
FT MOD RES 181 181 PHOSPHORYLATION (BY PKC).
FT MOD RES 204 204 PHOSPHORYLATION (BY PKC).
FT MOD RES 214 214 PHOSPHORYLATION (BY PKC).
SQ SEQUENCE 219 AA; 24710 MW; E4A882C1B7225FAP CRC64;
Query Match 6.3%; Score 131; DB 1; Length 219;
Best Local Similarity 26.2%; Pred. No. 0.0011;
Matches 42; Conservative 27; Mismatches 73; Indels 18; Gaps 5;
QY 141 KELMVHVGGLIQMCCVQSTF-VKHVTKVVEIFSGRRAKERIVFYHKLMSVEYSQS 199
DB 7 KEVHGAVGSGQVTLHCFSWSEWSDLSFTWRYQPEGRDAISIFHYAK--GQPYIDEV 63
QY 200 GHFQNRVNLVGDIFRNDGSIHQVRESDDGNYTCSIHLGNLVFKKT--IVLHVSPEEP 257
DB 64 GTFKERIQWGDPRKDGSIHNLVDYSDNGTFTCDVKNPPDIIVGKTSQVTLVYFVKVPT 123
QY 258 TLVTPAALRPLVLGNQNLVIIVGIVCATILLPVLIVK 297
DB 124 RY-----GVVLGA-----VIGGILGVLLALLLFYLIR 151
RESULT 12
MYP0_MOUSE
ID MYP0_MOUSE STANDARD; PRT; 248 AA.
AC P21573;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin P0 protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).
DE MPZ OR P0.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9124320; PubMed=1709914;
RA You K.H., Hsieh C.L., Hayes C., Stahl N., Francke U., Popko B.;
RT "DNA sequence, genomic organization, and chromosomal localization of the mouse peripheral myelin protein zero gene: identification of polymorphic alleles";

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FT HELIX      105      107
FT TURN      108      108
FT STRAND    109      109
FT STRAND    112      114
FT STRAND    119      121
FT STRAND    123      130
FT STRAND    138      147
SQ SEQUENCE  248 AA;  BB703F173466119B CRC64;

Query Match
Best Local Similarity  6.3%; Score 130; DB 1; Length 248;
Matches 43; Conservative 32; Mismatches 74; Indels 22; Gaps 6

QY 130 AVLHLVLPPEPKELMVHVGGLIQGCVFQSTE-VKHWTKVWIFSGRRAKGEIVFRYHK 188
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 29 AIVVTV---DREVVGAVGQVTLHCSFWSSEWSDDISFTWRVQPEGGRDAISIFHYAK 84
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 189 LRMSVEVSQSHGFQNRVNLVGDITFRNDGSLMLOQVRESDGNGYTCSHLGNLVFKKT-- 246
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 85 ---GQPYIDEVGTGFKERIQWYDPSWKDGSIVIHNLDSYDNGTFTCDVKNPDPVGVKTSQ 141
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 247 IVLHVSPEEPRTLTPAALRPLVLGGNQLVIIVGIVCATILLPVLILIVK 297
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 142 VTLVFEKVTRY-----GVVLGA-----VIGGILGWLLLLLLFYLR 180
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
A33_HUMAN
ID_A33_HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
OS GPA33.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID:9606;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TI TISSUE-Colon carcinoma;
RX MEDLINE=97165045; PubMed=9012807;
RA Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.;
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily";
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
[2]
POST-TRANSLATIONAL MODIFICATIONS.
RP MEDLINE=97396159; PubMed=9245713;
RX Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.;
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium.";
RL Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC CARBOHYDRATE.
CC -!- PTM: Palmitoylated.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC or send an email to license@isb-sib.ch).

CC EMBL; U79725; AAC50957.1; --
DR Genew; HGNC:4445; GPA33.
DR MIM; 602171; --
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319 CELL SURFACE A33 ANTIGEN.
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 319 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 134 IG-LIKE V-TYPE.
FT DOMAIN 140 227 IG-LIKE C2-TYPE.
FT DOMAIN 258 261 POLY-CYS.
FT DISULFID 43 117 POTENTIAL.
FT DISULFID 146 222 POTENTIAL.
FT DISULFID 162 211 POTENTIAL.
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7A9F45C2408E CRC64;

Query Match 6.2%; Score 128.5; DB 1; Length 319;

Best Local Similarity 21.1%; Pred. No. 0.003;
Matches 73; Conservative 51; Mismatches 141; Indels 81; Gaps 14;

Qy 23 LNVSPPE--LTVHVGDSSALMCVQSTEDKCFKIDMTLSPGEHAKDEYVLYYSNLSVP 80
Db 22 ISVETPDVLRASQKSVTLPTCTVHTSTSRGLIQMDKLLTHT-ERKVIWPFSSKNKYI 80
Qy 81 IGR-FQNRVHLMGDILCNDGSLILQDVQEAQGTVCIR----LKGESQVFKKAVLVHV 135
Db 81 HGEYKRVSVTSNNAEQSDASITDILTADNGIYECVSLMSDLGNKTSRVLVLV-V 139
Qy 136 LPBPK---ELMVHVGGLIQMGVQSTEVKHTVKVEMIFSGRAKEIVFRTYHKLMS 192
Db 140 PPSKPECGIEGETIIGNNIQLTC--QSKGSGPTQYSW-----KRYNLNOE 184
Qy 193 VEYSQSWGHFQNRVNLVGDIFRNDGSIMLQVRESDGNYTCSIHLGNLVFKKTVLHVS 252
Db 185 QPLAQP-----ASQPVSLSKNISTDTSGYICT-----S 213
Qy 253 PREPTLT---VTPAALRPLVLGGNOLVIVGIVCATILLPVLILVKKTCGNKSSVNST 309
Db 214 SNEGTQCNITVAVRSPMVALVGVAVGVAII--IGIIYCCCGKGDNDTE 270
Qy 310 VLVKNTKNTNPKIKPKCHFERCEGKHYSPIIVREVBEEBPE 355
Db 271 ---KEDAPNRYAEYEP-----PEQLRELSRENEED 299

RESULT 15

IPL2 HUMAN
ID IPL2 HUMAN STANDARD; PRT; 686 AA.
AC Q9NP60; Q9NZNO;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE X-linked interleukin-1 receptor accessory protein-like 2 precursor
DE (ILIRAPL-2 related protein) (Interleukin-1 receptor 9) (IL-1R) (IL-1
DE receptor accessory protein-like 2) (Three immunoglobulin domain-
DE containing IL-1 receptor-related 1) (TIGIR-1).

GN ILIRAPL2 OR ILIR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RP TISSUE=Petal brain;
RC MEDLINE=20487552; PubMed=1031108;
RX Sana T.R., Debets R., Timans J.C., Bazan J.F., Kastelein R.A.;
RT "Computational identification, cloning, and characterization of
IL-1R9, a novel interleukin-1 receptor-like gene encoded over an
RT unusually large interval of human chromosome Xq22.2-q22.3.";
RL Genomics 69:252-262(2000).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=20459050; PubMed=10882729;
RC Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S.,
RA Sims J.E.;
RT "Identification and characterization of two members of a novel class
of the interleukin-1 receptor (IL-1R) family. Delineation of a new
RT class of IL-1R-related proteins based on signaling.";
RL J. Biol. Chem. 275:29946-29954(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Grabowski M., Lorenz B., Hubel R., Strom T.M.;
RT "A gene (ILIRAPL-2) with 61% identity to ILIRAPL maps to Xq22.2.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=21472256; PubMed=11587848;
RA Ferrante M.I., Ghiani M., Bulfone A., Franco B.;
RT "ILIRAPL2 maps to Xq22 and is specifically expressed in the central
RT nervous system.";
RL Gene 275:217-221(2001).
RN [5]
RP SEQUENCE OF 29-686 FROM N.A.
RX MEDLINE=20218565; PubMed=10757639;
RA Jin H., Visswesvaran R., Gardner R.J., Roberts R.G.;
RT "Two novel members of the interleukin-1 receptor gene family, one
RT deleted in Xp21.3-Xp21.3 mental retardation.";
RL Eur. J. Hum. Genet. 8:87-94(2000).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! TISSUE SPECIFICITY: Detected at low levels in fetal and adult
CC brain, in particular in the frontal lobe, temporal lobe and fetal
CC cerebellum. Detected at very low levels in skin, liver, fetal
CC ovary and in placenta.
CC -! SIMILARITY: Belongs to the interleukin-1 receptor family.
CC -! SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -! SIMILARITY: Contains 1 TIR domain.
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CC EMBL; AF212016; AAF61307.1; --
DR EMBL; AF284436; AAG21370.1; --
DR EMBL; AJ272208; CAB86868.1; --
DR EMBL; AJ290436; CAB89867.1; --
DR EMBL; AF181285; AAF59412.1; --
DR Genew; HGNC:5997; ILIRAPL2.
DR MIM; 300277; --
DR GO; GO:0004908; F:interleukin-1 receptor activity; TAS.
DR GO; GO:0007417; P:central nervous system development; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.

Search completed: March 15, 2004, 08:34:38
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 08:31:44 ; Search time 45 Seconds
(without alignments)
2762.537 Million cell updates/sec

Title: US-09-997-514-422

Perfect score: 2067

Sequence: 1 MFCPLKLLPVLDDYSLG.....RNNSLEKSGGMPKTTQAF 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2067	100.0	394	4	Q86YT9
2	1985	96.0	384	4	Q8N917
3	1783	86.3	394	4	Q7Z499
4	1364	66.0	283	4	Q8NF70
5	982	47.5	379	11	Q8OUL9
6	198	9.6	335	13	Q9YGV5
7	192	9.3	335	13	Q9PWR4
8	191	9.2	335	13	Q9YGH1
9	183	8.9	365	6	Q8MWV3
10	168	8.1	344	4	Q9UKV4
11	167	8.1	2828	4	Q9NR99
12	164	7.9	319	6	Q9TU80
13	158	7.6	373	4	Q9H6B4
14	154.5	7.5	373	11	Q920S5
15	152.5	7.4	372	11	Q8K1G0
16	152	7.4	319	6	Q9TU79
					Q86YT9 sus scrofa

17	151.5	7.3	437	13	Q90WI4	Q90wi4 gallus gall
18	151	7.3	372	13	Q90Y50	Q90y50 brachydanio
19	150.5	7.3	373	11	Q8R373	Q8r373 mus musculus
20	147.5	7.1	243	4	Q9UEL4	Q9uel4 homo sapien
21	147.5	7.1	269	4	Q95297	Q95297 homo sapien
22	147	7.1	330	11	P97269	P97269 cavia porce
23	147	7.1	344	11	Q9R067	Q9r067 rattus norv
24	147	7.1	358	11	Q9R066	Q9r066 rattus norv
25	147	7.1	584	4	Q9Y3Y8	Q9y3y8 homo sapien
26	146	7.1	352	11	Q91W66	Q91w66 mus musculus
27	146	7.1	365	11	Q9DBJ8	Q9dbj8 mus musculus
28	144.5	7.0	183	4	Q9UEL6	Q9uel6 homo sapien
29	144.5	7.0	209	4	Q9NYK4	Q9nyk4 homo sapien
30	142.5	6.9	202	4	Q8IX11	Q8ix11 homo sapien
31	142	6.9	337	11	P97268	P97268 cavia porce
32	140	6.8	215	11	Q91WI4	Q91wi4 mus musculus
33	139.5	6.7	329	13	Q9IAY6	Q9iay6 mus musculus
34	138.5	6.7	318	13	Q91664	Q91664 xenopus lae
35	137.5	6.7	907	5	Q9NEG0	Q9neg0 drosophila
36	137.5	6.7	3215	5	Q8IRV7	Q8irv7 drosophila
37	137.5	6.7	4117	5	Q8IRV9	Q8irv9 drosophila
38	137.5	6.7	4179	5	Q9W4V4	Q9w4v4 drosophila
39	137.5	6.7	4223	5	Q8MEN3	Q8mpn3 drosophila
40	137.5	6.7	4228	5	Q8IRV8	Q8irv8 drosophila
41	136	6.6	338	4	Q8IV49	Q8iv49 homo sapien
42	136	6.6	339	13	Q9IAZ1	Q9iazi spherooides
43	135.5	6.6	199	13	Q8JG36	Q8jg36 brachydanio
44	134.5	6.5	403	6	Q9N2H5	Q9n2h5 equus cabal
45	134	6.5	252	4	Q8WWT6	Q8wwt6 homo sapien

ALIGNMENTS

RESULT 1

Q86YT9 PRELIMINARY; PRT; 394 AA.
AC Q86YT9
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adhesion molecule AMICA.
GN AMICA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Foster J.S., Gurney A.L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY138965; AAN52117.1; --
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 2.
DR PROSITE; P550835; IG_LIKE; 2.
SQ SEQUENCE 394 AA; 44339 MW; 64B542P9384C7642 CRC64;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFCPLKLLPVLDDYSLGLNDLVNVP	ELTVHVGDSALMGCVFQSTEDKCI	FKDKIDWTLS 60
Db	1	MFCPLKLLPVLDDYSLGLNDLVNVP	ELTVHVGDSALMGCVFQSTEDKCI	FKDKIDWTLS 60
QY	61	PGEHAKDEVLYYYNLSVPIGRFQNR	VHLMGDIICNDGSLLLQDVQEA	DQQTTCYICEIRL 120
Db	61	PGEHAKDEVLYYYNLSVPIGRFQNR	VHLMGDIICNDGSLLLQDVQEA	DQQTTCYICEIRL 120
QY	121	KGESOVFKKAVLHVLPPEPKELMHV	GLTQMGCVFQSTEVKHVTKVEW	IFSGRAKKE 180
Db	121	KGESOVFKKAVLHVLPPEPKELMHV	GLTQMGCVFQSTEVKHVTKVEW	IFSGRAKKE 180

Db	245	EPRTLVTTPAALRPLVLGGNQLVLIIGVIVCATILLPVLILIVKKTGCKNKSNSVNSTVLVKN	304
Qy	315	TKTNPKEIKKPCHEKCEKHIYSPILVREVEEPESEKSEATVMTMHPVWPSLRSD	374
Db	305	TKTNPKEIKKPCHEKCEKHIYSPILVREVEEPESEKSEATVMTMHPVWPSLRSD	364
Qy	375	RNNSLEKSGGMPKTOQAF	394
Db	365	RNNSLEKSGGMPKTOQAF	384
RESULT 3			
Q7Z499			
ID	Q7Z499	PRELIMINARY; PRT; 394 AA.	
AC	Q7Z499	01-OCT-2003 (TREMBlrel. 25, Created)	
DT	01-OCT-2003	(TREMBlrel. 25, Last sequence update)	
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)	
DE	Putative junctional adhesion molecule precursor.		
GN	JAML.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Bone marrow;		
RA	Moog-Lutz C., Cave-Riant F., Guibal F.C., Breau M., Di Gioia Y.,		
RA	Cayre Y.E., Lutz P.G.;		
RT	"JAML, a novel protein induced in myeloid leukemia cells, has		
RT	characteristics of a junctional adhesion molecule.";		
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ515553; CAD56620.1; -.		
KW	Signal.		
FT	SIGNAL 1 19 Potential.		
FT	CHAIN 20 394 putative junctional adhesion molecule.		
SQ	SEQUENCE 394 AA; 43731 MW; B81F99C929D80C53 CRC64;		
Query Match 86.3%; Score 1783; DB 4; Length 394;			
Best Local Similarity 87.0%; Pred. No. 3.7e-155;			
Matches 354; Conservative 7; Mismatches 20; Indels 26; Gaps 4;			
Qy	1	MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLS	60
Db	1	MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLS	60
Qy	61	PGEHAKDEVLYYYNSLSPVPIGRFQNRVHLMGDIICNDGSLLIQDVQEADQGTIICEIRL	120
Db	61	PGEHAKDEVLYYYNSLSPVPIGRFQNRVHLMGDIICNDGSLLIQDVQEADQGTIICEIRL	120
Qy	121	KGESQVFKKAVVLHVLPEEPKELMHVGGIIQMGCVFQSTEVKHTVKEVIFSGRAKEE	180
Db	121	KGESQVFKKAVVLHVLPEEPKELMHVGGIIQMGCVFQSTQ-----DGAQ-RRR	168
Qy	181	IVF-----RYYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMQGVRES	227
Db	169	LYFVTTTNSGCLRSTPRAGATSRIGSE-TRDQGRMDIFVNLVGDIFRNDGSLMQGVRES	227
Qy	228	DGNYTCSIHLGNLVFKKTVLHVSPPEPTLTTPAALRPLVLGGNQLVLIIGVIVCATIL	287
Db	228	DGNYTCSIHLGNLVFKKTVLHVSPPEPTLTTPAALRPLVLGGNQLVLIIGVIVCATIL	287
Qy	288	LLPVLILIVKKTGCKNKSNSVNSTVLVKNKTNPKEIKKPCHEKCEKHIYSPILVREV	347
Db	288	LLPVLILIVKKTGCKNKSNSVNSTVLVKNKTNPKEIKKPCHEKCEKHIYSPILVREV	347
Qy	348	IEEPESEKSEATVMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF	394
Db	348	IEEPESEKSEATVMTMHPVWPSLRDRNNSLEKSGGMPKTOQAF	394
RESULT 4			
Q8NF70			
Db	245	EPRTLVTTPAALRPLVLGGNQLVLIIGVIVCATILLPVLILIVKKTGCKNKSNSVNSTVLVKN	304
Qy	315	TKTNPKEIKKPCHEKCEKHIYSPILVREVEEPESEKSEATVMTMHPVWPSLRSD	374
Db	305	TKTNPKEIKKPCHEKCEKHIYSPILVREVEEPESEKSEATVMTMHPVWPSLRSD	364
Qy	375	RNNSLEKSGGMPKTOQAF	394
Db	365	RNNSLEKSGGMPKTOQAF	384
RESULT 2			
Q8N917			
ID	Q8N917	PRELIMINARY; PRT; 384 AA.	
AC	Q8N917	01-OCT-2002 (TREMBlrel. 22, Created)	
DT	01-OCT-2002	(TREMBlrel. 22, Last sequence update)	
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)	
DE	Hypothetical protein FLJ37080.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Cerebellum;		
RA	Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,		
RA	Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,		
RA	Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,		
RA	Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,		
RA	Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,		
RA	Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,		
RA	Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,		
RA	Masuho Y., Nagai K., Isogai T.;		
RT	"NEDO human cDNA sequencing project.";		
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AK094399; BAC04347.1; -.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	SMART; SM00409; IG; 2.		
DR	PROSITE; PS50835; IG-LIKE; 2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 384 AA; 43091 MW; C93D8EF6C97B6591 CRC64;		
Query Match 96.0%; Score 1985; DB 4; Length 384;			
Best Local Similarity 99.5%; Pred. No. 1e-173;			
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	15	DYSLGLDNLVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLSPGEHAKDEVLYYY	74
Db	5	DYSLGLDNLVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLSPGEHAKDEVLYYY	64
Qy	75	SNLSVPIGRFQNRVHLMGDIICNDGSLLIQDVQEADQGTICEIRLKGESQVFKKAVVLH	134
Db	65	SNLSVPIGRFQNRVHLMGDIICNDGSLLIQDVQEADQGTICEIRLKGESQVFKKAVVLH	124
Qy	135	VLPEEPKELMHVGGIIQMGCVFQSTEVKHTVKEVIFSGRAKEEIVFRYHKLMSVE	194
Db	125	VLPEEPKELMHVGGIIQMGCVFQSTEVKHTVKEVIFSGRAKEEIVFRYHKLMSAE	184
Qy	195	YSQSWGHFQNRVNLVGDIFRNDGSLMQVRSDDGNYTCSIHLGNLVPKTIIVHVSPE	254
Db	185	YSQSWGHFQNRVNLVGDIFRNDGSLMQVRSDDGNYTCSIHLGNLVPKTIIVHVSPE	244
Qy	255	EPRTLVTTPAALRPLVLGGNQLVLIIGVIVCATILLPVLILIVKKTGCKNKSNSVNSTVLVKN	314

ID Q8NF70 PRELIMINARY; PRT; 283 AA.
 AC Q8NF70;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FLJ00300 protein (Fragment).
 GN FLJ00300.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
 RT "The nucleotide sequence of a long cDNA clone isolated from human
 spleen.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK090409; BAC03390.1; -;
 DR InterPro; IPR003599; IG.
 DR SMART; SM00409; IG-like.
 DR PROSITE; PS50835; IG-LIKE; 2.
 FT NON_TER.
 SQ SEQUENCE 283 AA; 32079 MW; CCACB5B0839BB30E CRC64;
 Query Match 66.0%; Score 1364; DB 4; Length 283;
 Best Local Similarity 99.2%; Pred. No. 7.3e-117;
 Matches 257; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTL 60
 DB 25 MFCPLKLLPVLDDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTL 84
 QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGYTCIRL 120
 DB 85 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGYTCIRL 144
 QY 121 KGSQVFKKAVLVLPPEEPKELMVHVGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 180
 DB 145 KGSQVFKKAVLVLPPEEPKELMVHVGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE 204
 QY 181 IVFRYHKLMSVEYQSQWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 240
 DB 205 IVFRYHKLMSVEYQSQWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSIHLGN 264
 QY 241 LVFPKTIVLVHVSPEEPTL 259
 DB 265 LVFPKTIVLVHVSPEEPTL 283
 RESULT 5
 Q8OUL9 PRELIMINARY; PRT; 379 AA.
 ID Q8OUL9
 AC Q8OUL9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to adhesion molecule AMCA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B5/BGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell;
 RA Strausberg R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC050133; AAH50133.1; -;
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG-LIKE; 2.
 SQ SEQUENCE 379 AA; 42561 MW; 2CC0F2987CB12B7F CRC64;
 Query Match 47.5%; Score 982; DB 11; Length 379;
 Best Local Similarity 56.1%; Pred. No. 1.3e-81;
 Matches 222; Conservative 35; Mismatches 105; Indels 34; Gaps 9;
 QY 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDW 57
 DB 1 MFCPLKLLPVLDDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDW 60
 QY 58 TLSPEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGYTCIRL 117
 DB 61 TFSKDDKDDASEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGYTCIRL 120
 QY 118 IRLKGSQVFKKAVLVLPPEEPKELMVHVGLIQMGCVFQSTEVKHVTKVEWIF-SGRR 176
 DB 121 IRLKGSQVFKKAVLVLPPEEPKELMVHVGLIQMGCVFQSTEVKHVTKVEWIF-SGRR 180
 QY 177 AKEEIVFRYHKLMSVEYQSQWGHFQNRVNLVGDIFRNDGSIIMLQGVRESGGNYTCSI 236
 DB 181 TEETVLSYDSNNRSG--KFQSLGRFRNRVLDLTGDISRNDGSIKLTQVKESDRGTYTCSI 238
 QY 237 HLGNLVFKKTIIVLVHVSPEEPTLIVPAALRPL-----VLGGNQLVIVGVTCATILLP 290
 DB 239 YVGLKSEKTIIVLVHVSPEEPTLIVPAALRPL-----VLGGNQLVIVGVTCATILLP 296
 QY 291 VLLIVVKTCKNKSSVNSTVLVK---NTKTNPEIKPKCHFERCEGEKHYSPILVREV 347
 DB 297 VLLIVVKTCKNKSSVNSTVLVK---NTKTNPEIKPKCHFERCEGEKHYSPILVREV 342
 QY 348 IEEEPSEKSEAYVMTMHPVWPSLRSDRNNLSLEKS 383
 DB 343 TERGISGE-SEGTYMTMNPVWPS--SPKASSLVRS 375
 RESULT 6
 Q9YGV5 PRELIMINARY; PRT; 335 AA.
 ID Q9YGV5
 AC Q9YGV5;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cht1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077161; PubMed=9862345;
 RA Chretien I., Marcuz A., Courtet M., Katevuo K., Vainio O., Heath J.K.,
 RA White S.J., Du Pasquier L.;
 RT "CTX, a Xenopus thymocyte receptor, defines a molecular family
 conserved throughout vertebrates.";
 RL Eur. J. Immunol. 28:4094-4104(1998).
 DR EMBL; AF061023; AADI7523.1; -;
 DR HSSP; P06907; 1NEU.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 2.
 SQ SEQUENCE 335 AA; 36561 MW; 071A313C3CE6DCA0 CRC64;
 Query Match 9.6%; Score 198; DB 13; Length 335;
 Best Local Similarity 22.1%; Pred. No. 1.2e-09;
 Matches 88; Conservative 74; Mismatches 158; Indels 78; Gaps 17;

QY	1	MFCLPLKLLPVLDDYSLGLNDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIFKIDWT	58
Db	1	MF-PTMLKIFPILATLAGHVRGVVTVPEKTVNVKGTGNATLLCTYTSSQPLGNFFIQWS	59
QY	59	LSPEGHAKDEYVLYYSNLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQEOAGQTYICEI	118
Db	60	FYSAKESQLHTIYYISGQSYSGYGEFKDRI--TAATSPGNASITISNMQPSDTGSYTCEV	117
QY	119	RL-----KGESQVFKKAVLHVL--PEEP---KELMVHVGGLIOMGCVFQSTEVKHHVTKVE	169
Db	118	FSPQDDAGOSQ---KSVIVNLVKPSKPFCKIEGTPKKGHLIYLLCKCDQ--GLPHPT---	170
QY	170	WIFSGRAKEBEIVFRYYHKLMSVEYSQSMGHFQNRVNLVGDIFRNDGSIMLQ--VRES	228
Db	171	-----YRWY-----KVD-----ENTLTPTEYFNPDTGILYIGNLTTFE	204
QY	229	GGNYTCSIHLGNLVFKKTIIVLHVSPEEPTLVTAAALRPLVLGNGQLVIIVGIVCATILL	288
Db	205	TGHYRCI--ASNIMGNSTCELDLTSMSHSDGNIVAGAL-----IGAILAAVII	249
QY	289	LPVLILIVKTCGKSSVNSTVLVKNTKTNPEIKPKPCHPERCEGKHIYSPITIVREVI	348
Db	250	CAIIVVLTAKKKKSSNE--MQVMAQKQSNAEYAQVP-----NEENTPQPAVLPSNA	301
QY	349	EEEEPEKSEATYTMHPVWPSLSRSDRNSLEKSGGG	386
Db	302	TNEQPSADEAASETP-----ENDEKHEVQKEETAG	332
RESULT 7			
Q9PWR4	ID	Q9PWR4	PRELIMINARY; PRT; 335 AA.
AC	Q9PWR4;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Chrl thymocyte antigen precursor.		
GN	Chrl.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=H.B19; TISSUE=Thymus;		
RA	Katevuo K.H., Boyd R., Gobel T.T., Bean A., Dunon D., Imhof B.A.,		
RA	Vainio O.;		
RT	"Chrl, a new IgSF member inhibits thymocyte differentiation at the		
RT	double positive stage.";		
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; Y14064; CAA74391.1; -.		
DR	HSSP; P06907; INEU.		
DR	InterPro; IPR007110; Ig-like.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 2.		
KW	Signal.		
FT	CHAIN	1 21	POTENTIAL.
FT	CHAIN	22 335	CHTL THYMOCYTE ANTIGEN.
SQ	SEQUENCE	335 AA; 36509 MW; AA6159598079B438	CRC64;
Query Match			
Best Local Similarity 9.3%; Score 192; DB 13; Length 335;			
Matches 88; Conservative 76; Mismatches 156; Indels 78; Gaps 18;			
QY	1	MFCLPLKLLPVLDDYSLGLNDLNVSPPELTVHV--GDSALMGCVFQSTEDKCIFKIDWT	58
Db	1	MF-PTMLKIFPILATLAGHVRGVVTVPEKTVNVKGTGNATLLCTYTSSQPLGNFFIQWS	59
QY	59	LSPEGHAKDEYVLYYSNLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQEOAGQTYICEI	118
Db	60	FYSAKESQLHTIYYISGQSYSGYGEFKDRI--TAATSPGNASITISNMQPSDTGSYTCEV	117
QY	119	RL-----KGESQVFKKAVLHVL--PEEP---KELMVHVGGLIOMGCVFQSTEVKHHVTKVE	169
Db	118	FSPQDDAGOSQ---KSVIVNLVKPSKPFCKIEGTPKKGHLIYLLCKCDQ--GLPHPT---	170

Query Match		8.9%;	Score 183;	DB 6;	Length 365;
Best Local Similarity		23.9%;	Pred. No. 3.le-08;		
Matches		95;	Conservative 61;	Mismatches 146;	Indels 96; Gaps 20;
QY	5	LKLLLPVLLDYSGLNDLNVSPETVH--VGDSALMGCVFQ-STEDKCFIKIDWTLSP	61		
Db		: :			
	5	LRPLLCCGVADFTRG---LSITTFEQMIERAKGETAYLPCKFTLGPEDGQLDIEMLLSP	61		
QY	62	GHAKEDEYLVXYNSLNVPVIGRQN---RVHL-MGDILCNDGSLLODVGEADQGYICE	117		
Db		: :			
	62	AONQKVDQVILLYSGDKIVDDYYQDLKGRVHFNTSNLKGSDASINTVNLQISDIGTYQCK	121		
QY	118	IRLKGESQVFKAVALHVLFEEPEKELMHVGGLIOMGCVFQSTEVKHVTKVWEIFSGRA	177		
Db		: :			
	122	V--KKAPGVGNKKIQLTVL-VKPSGRCYVDGSEEGNDFK-----LKCE-----P	164		
QY	178	KE-EIVFRY-YHKLMMSVEYSQGWHGFQRVNVLVGDIPFRNDGSIMLQGVRESDGNGYTCS	235		
Db		: :			
	165	KESGPLRYEWOXKLSDSKLPTSW----LPMTSPV-----ISVKNASAEYSGYTCT	213		
QY	236	IHLGNLVFKTKTVLHVSPPEEPRLTVTPAALRPVLVCGNQVLVIIVGVICATILLPLPVILI	295		
Db		: :			
	214	VR--NEVGSQCCLRLLRDVVPP-----SNRAGTTAGAVIGTLIAL-VLIAI	255		

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QY      5 LKULILPVLLDYSLGULNDLNVSPELTVH--VGDSALMGCVFO-STEDKCIFKIDMTLSF 61
Db      5 LCFVILLGVVDFA--RSLTITPEEMI EKAKGETAYLPCKFTLSPEDQGLDIEWLISF 61
QY     62 GEBAKEBYLVYYSNLSVPIGRF---QNRVHL-MGDILCNDGSLLODVQEAQGTVICE 117
Db     62 ADNQKDQVILLYSGDKIYDDYPDLUKGRVHFTSNDLKSGDASINTNLQLSDIGTYQCK 121
QY    118 IRLKGESQVFKAWLIHLVLPEEPKELMHVGGELIQMCVF---QSTEVKHVTWKVEWIFS 173
Db    122 V--KKAPGVANKIHLVL-VKPSGARCYDGSSEI GSFKI KCEPKESGLPQYEW--- 175
QY    174 GRRAKEEIVFRYHHKLMSVEYSQSHGFQNRVNLVGDIFRNDSIMLQVRESDGNYT 233
Db    176 -----QKLSDSQKMPTSW-----LAEMTSSV-----LSVKNASSEYSGTVS 211
QY    234 CSTHLGNLYFKKTI VLHVSPFEPRTLVTPAALRPVLVGGNQLVII GVICATILLPLVLI 293
Db    212 CTVR--NRVGSQCCLRLNVWPP-----SNKAGLTAGAIIGTLTALLALIG 254
QY    294 LIVKKT CGNKSSVNSTVL VKNTKTNPEIKKPCHFERCEGEKHIYSPIIVREVIEEEP 353
Db    255 LI-I-PCC-----RKRRREKYKEVHH-----IREDPV 282
QY    354 SEKSATYTMHPVNPWSLRSDNN--SLEKSGGGMPKTQ 391

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Db 283 PPKSRTSTARS;-----IGSNHSSLSGMSPSNMEGYSKTQ 317

RESULT 11

Q9NR99 PRELIMINARY; PRT; 2828 AA.
AC Q9NR99;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Adlican.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta.
RA Crowl R.M., Luk D.;
RT "Identification of the gene encoding Adlican, a novel protein
RT expressed in human arthritic tissues."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF245505; AAF86402.1; -.
DR HSP; P56276; 1TLK.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00047; Ig; 12.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF01463; LRRCT; 1.
DR SMART; SM00408; IGC2; 10.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 3.
DR PROSITE; PS50835; IG_LIKE; 12.
KW Immunoglobulin domain.
SQ SEQUENCE 2828 AA; 312291 MW; A18377D8554F1FE1 CRC64;

Query Match 8.1%; Score 167; DB 4; Length 2828;
Best Local Similarity 21.8%; Pred. No. 1.5e-05;
Matches 87; Conservative 74; Mismatches 149; Indels 90; Gaps 20;
QY 42 CVFQST--EDKCFIDWTLSPG--EHAKD-EYVLYYSNL-----SVP 80
Db 2221 CVARNKVGDDYVVLKVDVVMKPAKIEHKEENDHKVFYGGDLKVDCAVATGLPNEIWSLIP 2280
QY 81 IGRFONRVHLMGD-----ILCNDGSLLLQDVQEAQGTIYC--EIRL-KGESQVFK 129
Db 2281 DGLSVNFEQSDSGGRKRYVFNNGTLTFNEVGMBEGDYTCFAENQVGKDEMRVVK 2340
QY 130 AVLHLVPEEPKELMVHV--GGLIQMGCVFQSTEVKHTVKTVEIFSGRAKEEIVFRYYH 187
Db 2341 VTAPATNTKTYLAVQPYGVDVTVAC---EAKGEPKPVTVLSPNTKV----- 2387
QY 188 KLRMSVEYSQSMGHGFQNRVNLVGDIFRNDGSLMLQGVRESGNGTCSIHGLNLFVKTI 247
Db 2388 -IPTSESKYQIV-----QDTLLIQAKQRSDSGNTVCLVRNSAGEDRKIV 2431
QY 248 VLVHSPPEPRTLVTLP---AALPLVLGGNQIIV---IVGIVCATIL-LLPVLILVKKTC 300
Db 2432 WIHVNVQPKINGNPNPITTVREIAAGSGRKLIDCKAEGIPTRVLWAPPEGVWLPAPYY 2491
QY 301 GNKSSV--NSTVLVKNKTKTNPEIKPKCHPERCEGEKHIYSPPIVREIVEE---EEP-S 354
Db 2492 GNRITVHGNSLDIRSLRKS--DSVQIVCWARNEGGEARLIQVLTLPMEKPIFHDPIIS 2549
QY 355 EKSEATYMTMHPV-----WPSLRSDRNNLSLEKSG 384
Db 2550 EK--ITAMAGHTISLCSAAGTPTPSLVVWLPNGTDLQSG 2587

RESULT 12

Q9TU80 PRELIMINARY; PRT; 319 AA.
AC Q9TU80;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Coxackie-adenovirus-receptor homolog (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=bred German shepherd; TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109645; AAF01256.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
FT NON TER 319
SQ SEQUENCE 319 AA; 35422 MW; 85C63A6EC7986965 CRC64;

Query Match 7.9%; Score 164; DB 6; Length 319;
Best Local Similarity 22.6%; Pred. No. 1.4e-06;
Matches 91; Conservative 61; Mismatches 146; Indels 104; Gaps 19;
QY 5 LKLILLPVLIDYSLGLNDLVNVPPELTVH--VGDSALMGCVFQ-STEDKCFIDWTLSP 61
Db 5 LRFVLLCGVADFT---RSLSTTPEQWIEKAKGETAYLPCKFTLSPEQGLDIEMLSP 61
QY 62 GEHAKDEYLVYXYNLSVPIGRFQF---RVHL-MGDILCNDGSLLLQDVQEAQGTIYC 117
Db 62 ADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTLRLSDICTGYCK 121
QY 118 IRLKGESOVFKKAVLHVLPPEPKELMVHVGLIQMGCVF---QSTEVKHTVKTVEIF 173
Db 122 V--KKAPGVGNKKIQLTVL-VKPSGIRCYVDGSEIEGNDFKLKCEPKSGSLPLQYEW--- 175
QY 174 GRRAKEEIVFRYYHKLMSVEYSQSMGHGFQNRVNLVGDIFRNDGSLMLQGVRESGNGYT 233
Db 176 -----QKLSNSQKTPPSWS-----TMTSPV-----ISIKNASTEYGTI 211
QY 234 CSHILGNLFFVKTIIVLHVSPE--EPTLVTAPALPLVLGGNQIIVIGIVCATILLIPV 291
Db 212 C-----TVINRVGSDQCQLRLNVVPSNRAGTIAG---AVVG-----ILLALV 251
QY 292 LILIVKTKCGNKSNSVNTVLVKNKTKTNPEIKPKCHPERCEGEKHIYSPPIVREIVEE 351
Db 252 LIGTIVFC-----RKKRREEKYEVHH-----IRE 280
QY 352 EPSEKSEATYMTMHPVWPSLRSDRNN--SLEKKSGGMPKQTQ 391
Db 281 VPPLKSRSTARS;-----IGSNHSSLSGMSPSNMEGYSKTQ 317

RESULT 13

Q9H6B4 PRELIMINARY; PRT; 373 AA.
ID Q9H6B4
AC Q9H6B4;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2004, 08:27:54 ; Search time 58 Seconds
(without alignments)
1919.374 Million cell updates/sec

Title: US-09-997-514-422
Perfect score: 2067
Sequence: 1 MFCPLKLIILPVLVDYSLG.....RNSLEKSGGMPKQQA 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2067	100.0	394	3	AAY66764 Membrane-
2	2067	100.0	394	3	AAB33454 Human PRO
3	2067	100.0	394	3	AAY94452 Human inf
4	2067	100.0	394	3	AAB24433 Human PRO
5	2067	100.0	394	4	AAL12431 Human PRO
6	2067	100.0	394	4	AAM38860 Human pol
7	2067	100.0	394	4	AAB65287 Human PRO
8	2067	100.0	394	5	AAB83689 Human PRO
9	2067	100.0	394	5	ABB4933 Human PRO
10	2067	100.0	394	5	ABB95539 Human ang
11	2067	100.0	394	6	ABU58102 Human PRO
12	2067	100.0	394	6	ABU59180 Novel hum
13	2067	100.0	394	6	ABU82692 Human sec
14	2067	100.0	394	6	ABO17875 Novel hum
15	2067	100.0	394	6	ABU60611 Human sec
16	2067	100.0	394	6	ABU80836 Human PRO
17	2067	100.0	394	6	ABO33802 Novel hum
18	2067	100.0	394	6	ABU13993 Human PRO
19	2067	100.0	394	6	ABU81129 Human PRO
20	2067	100.0	394	6	ABU72578 Novel hum
21	2067	100.0	394	6	ABU66829 Human PRO
22	2067	100.0	394	6	ABU59910 Novel sec
23	2067	100.0	394	6	ABU59327 Human sec
24	2067	100.0	394	6	ABO26024 Human PRO
25	2067	100.0	394	6	ABO25100 Human sec

ALIGNMENTS

RESULT 1
AAY66764
ID AAY66764 standard; protein; 394 AA.
XX
AC AAY66764;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1387.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999. ✓
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 03-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.

Abu82145 Novel hum
Abu59033 Human sec
Abu92411 Novel hum
Abu59476 Novel hum
Abu67105 Human sec
Abu92242 Novel hum
Abu10948 Human PRO
Abu81700 Novel hum
Abu88639 Human sec
Abu34153 Human PRO
Ada46039 Novel hum
Ada76470 Human PRO
Abj72325 Human PRO
Ada19120 Human PRO
Ada61743 Homo sapi
Adb19528 Novel hum
Adb28069 Human PRO
Ada86548 Novel hum
Adb16112 Human PRO
Ada37933 Human sec

QY 61 PGEHAKDEYLVLYYNSLVPTGRFQNRVHLMGDIICNDGSLLLQDVQADQGTVCETRL 120
 DB 61 PGEHAKDEYLVLYYNSLVPTGRFQNRVHLMGDIICNDGSLLLQDVQADQGTVCETRL 120
 QY 121 KGESQVFKAIVLHVLPPEPKELMVHVGLIQMGCVFQSTEVKHVTKVWFSGRRAKEE 180
 DB 121 KGESQVFKAIVLHVLPPEPKELMVHVGLIQMGCVFQSTEVKHVTKVWFSGRRAKEE 180
 QY 181 IVERYYHKLMSVEYSOSGWHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSIHGN 240
 DB 181 IVERYYHKLMSVEYSOSGWHFQNRVNLVGDIFRNDGSLMLQGVRESDGNYTCSIHGN 240
 QY 241 LVFKKTIIVLHVSPEPRTLVTPAALPLVGLGNOLVIIVGIVCATILLPLVLIIVKTKC 300
 DB 241 LVFKKTIIVLHVSPEPRTLVTPAALPLVGLGNOLVIIVGIVCATILLPLVLIIVKTKC 300
 QY 301 GNKSSVNSTVLVKNKTKNPEIKPKCHFERCEGEKHIYSPIIIVREVEEPEPEKSEAT 360
 DB 301 GNKSSVNSTVLVKNKTKNPEIKPKCHFERCEGEKHIYSPIIIVREVEEPEPEKSEAT 360
 QY 361 YMTMHPVWPVPSLRSDRNNSLEKSGGMPKTOQAF 394
 DB 361 YMTMHPVWPVPSLRSDRNNSLEKSGGMPKTOQAF 394

RESULT 2
 AAB33454
 ID AAB33454 standard; protein; 394 AA.
 XX AAB33454;
 AC AAB33454;
 DT 29-JAN-2001 (first entry)
 XX Human PR01387 protein UNQ722 SEQ ID NO:187.
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatologic; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neutropic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX Homo sapiens.
 OS
 XX
 PN W0200053758-A2.
 XX
 PD 14-SEP-2000.
 XX
 XX 02-MAR-2000; 2000WO-US005841.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 12-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99US-0128849P.
 PR 28-APR-1999; 99WO-US008615.
 PR 04-MAY-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-0132371P.
 PR 02-JUN-1999; 99WO-US014287P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US000376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 Kabakoff RC, Iau Y, Pan J, Pennica D, Shelton DL, Smith V;
 Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan M;

WPI; 2000-572271/53.
 N-PSDB; AAC58619.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 82; 309pp; English.

The present invention describes sixty four human PRO proteins which can
 be used in the treatment of immune related diseases. The human PRO
 proteins, anti-PRO antibodies, agonists and antagonists are useful for
 treating and diagnosing immune related disorders. The disorders are
 selected from systemic lupus erythematosus, rheumatoid arthritis,
 osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 immune-mediated renal disease, demyelinating diseases of the central and
 peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 or immune-mediated skin diseases, allergic diseases, immunological
 diseases of the lung, and transplantation associated diseases including
 graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 represent PCR primers and hybridisation probes used in the isolation of
 human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 represent human PRO polynucleotide and protein sequences given in the
 exemplification of the present invention

Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 3; Length 394;

Best Local Similarity 100.0%; Pred. No. 5.1e-188; Indels 0; Gaps 0;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLVDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 DB 1 MFCPLKLLPVLVDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 QY 61 PGEHAKDEYLVLYYNSLVPTGRFQNRVHLMGDIICNDGSLLLQDVQADQGTVCETRL 120

Db	61	PGHAKDEYVLYYNSLVPIGRFQNRVHLMGDILCNDGSLLLQDVQVQADQGYICIRL	120
Qy	121	KGESQVFKKAVLHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKEVIFSGRAKEE	180
Db	121	KGESQVFKKAVLHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKEVIFSGRAKEE	180
Qy	181	IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIHLGN	240
Db	181	IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIHLGN	240
Qy	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNOLVIVGIVCATIILLPVLILIVKTC	300
Db	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNOLVIVGIVCATIILLPVLILIVKTC	300
Qy	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVIEEPEPEKSEAT	360
Db	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVIEEPEPEKSEAT	360
Qy	361	YMTMHPVWPSPSLRSDRNSLEKSGGMPKTOQAF	394
Db	361	YMTMHPVWPSPSLRSDRNSLEKSGGMPKTOQAF	394
RESULT 3			
AA	94452	AA94452 standard; protein; 394 AA.	
XX	AC	AA94452;	
XX	XX	11-SEP-2000 (first entry)	
XX	DT	Human inflammation associated protein #11.	
XX	DE	Inflammation; rheumatoid arthritis; Crohn's disease; asthma;	
XX	KW	multiple sclerosis; allergy; AIDS; diabetes mellitus antiinflammatory;	
XX	KW	gene therapy; human.	
XX	OS	Homo sapiens.	
XX	XX	WO200029574-A2.	
XX	XX	25-MAY-2000.	
XX	XX	04-NOV-1999; 99WO-US026234.	
XX	XX	18-NOV-1998; 98US-00195292.	
XX	PA	(INCY-) INCYTE PHARM INC.	
XX	PI	Walker MG, Volkmut W, Klingler TM;	
XX	DR	WPI; 2000-387787/33.	
XX	DR	N-PSDB; AAA27133.	
XX	PT	New human inflammation-associated polypeptide useful for diagnosis,	
XX	PT	prevention and treatment of inflammatory diseases comprises product of	
XX	XX	gene coexpressed with e.g. CD16, L-selectin and IP-30.	
XX	PS	Claim 4; Page 42-43; 43pp; English.	
XX	CC	Eleven novel inflammation-associated genes have been identified in cDNA	
XX	CC	libraries from various tissues. The genes were selected according to	
XX	CC	their coexpression with the known inflammation genes, CD16, L-selectin,	
XX	CC	Src-like adapter protein, IP-30, superoxide homoenzyme subunits, alpha-	
XX	CC	1-antitrypsin, C1q-A, 5-lipoxygenase activating protein and SRC family	
XX	CC	tyrosine kinase. The novel polynucleotides may be used in hybridization	
XX	CC	assays to diagnose a disease or condition associated with altered	
XX	CC	expression of the inflammation genes. Antibodies against the genes may be	
XX	CC	useful in compositions for the diagnosis and treatment of such diseases	
XX	CC	associated with inflammation including rheumatoid arthritis, Crohn's	
XX	CC	disease, multiple sclerosis, AIDS, diabetes mellitus, asthma and allergy.	
XX	CC	Additionally the polynucleotides of the invention may be used for gene	
XX	CC	therapy. The present sequence is human inflammation associated protein	
CC	XX	#11, derived from Incyte Clone 3507924	
XX	XX	Sequence 394 AA;	
XX	XX	Query Match 100.0%; Score 2067; DB 3; Length 394;	
XX	XX	Best Local Similarity 100.0%; Pred. NO. 5.1e-188;	
XX	XX	Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MFCEPLKILLLPVLLDYSGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIFKIDWTLS	60
Db	1	MFCEPLKILLLPVLLDYSGLNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIFKIDWTLS	60
Qy	61	PGHAKDEYVLYYNSLVPIGRFQNRVHLMGDILCNDGSLLLQDVQVQADQGYICIRL	120
Db	61	PGHAKDEYVLYYNSLVPIGRFQNRVHLMGDILCNDGSLLLQDVQVQADQGYICIRL	120
Qy	121	KGESQVFKKAVLHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKEVIFSGRAKEE	180
Db	121	KGESQVFKKAVLHLVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKEVIFSGRAKEE	180
Qy	181	IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIHLGN	240
Db	181	IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIIMQGVRESGGNYTCSIHLGN	240
Qy	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNOLVIVGIVCATIILLPVLILIVKTC	300
Db	241	LVFKKTIHLVSPPEPRTLTPAALRPLVLGGNOLVIVGIVCATIILLPVLILIVKTC	300
Qy	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVIEEPEPEKSEAT	360
Db	301	GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIIVREVIEEPEPEKSEAT	360
Qy	361	YMTMHPVWPSPSLRSDRNSLEKSGGMPKTOQAF	394
Db	361	YMTMHPVWPSPSLRSDRNSLEKSGGMPKTOQAF	394
RESULT 4			
AA	24433	AAB24433 standard; protein; 394 AA.	
XX	AC	AAB24433;	
XX	XX	07-NOV-2000 (first entry)	
XX	DT	Human PRO1387 protein sequence SEQ ID NO:220.	
XX	DE	Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;	
XX	KW	diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;	
XX	KW	angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;	
XX	KW	cytostatic; gene therapy; vaccine.	
XX	OS	Homo sapiens.	
XX	XX	WO200032221-A2.	
XX	XX	08-JUN-2000.	
XX	XX	30-NOV-1999; 99WO-US028313.	
XX	XX	01-DEC-1998; 98WO-US025108.	
XX	XX	16-DEC-1998; 98US-0112850P.	
XX	XX	12-JAN-1999; 98US-0115554P.	
XX	XX	08-MAR-1999; 99WO-US005028.	
XX	XX	12-MAR-1999; 99US-0123957P.	
XX	XX	28-APR-1999; 99US-0131445P.	
XX	XX	14-MAY-1999; 99US-0134287P.	
XX	XX	02-JUN-1999; 99WO-US012252.	
XX	XX	23-JUN-1999; 99US-0141037P.	
XX	XX	20-JUL-1999; 99US-0144758P.	
XX	XX	26-JUL-1999; 99US-0145698P.	
XX	XX	01-SEP-1999; 99WO-US020111.	
XX	XX	08-SEP-1999; 99WO-US020594.	

PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
 PI Smith V, Watanabe CK, Williams PM, Wood WI;
 XX WPI; 2000-412154/35.
 DR N-PSDB; AAA77683.
 XX
 XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 PT and treating disorders of cardiovascular, endothelial or angiogenic
 PT disorders in mammals.
 XX
 XX Claim 72; Fig 92; 315pp; English.
 XX
 CC The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders of
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the prevention,
 CC treatment and diagnosis of diseases associated with inappropriate PRO
 CC expression such as cardiovascular, endothelial or angiogenic disorders in
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
 CC example, the nucleic acids (NCs) and vectors containing them and the PRO
 CC polypeptide may be used to treat disorders associated with decreased PRO
 CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
 CC nucleotide and protein sequences used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 394 AA;

 Query Match 100.0%; Score 2067; DB 3; Length 394;
 Best Local Similarity 100.0%; Pred. No. 5.1e-188;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MFCPKLILPVLDDYSLGNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLS 60
 Db 1 MFCPKLILPVLDDYSLGNDLNVSPPELTVHVGDLSALMGCVFQSTEDKCIKIDWTLS 60

 QY 61 PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDIILNDGSLLLQDVQADQGTVCIRL 120
 Db 61 PGEHAKDEYVLYYSNLSVPIGRFQNRVHLMGDIILNDGSLLLQDVQADQGTVCIRL 120

 QY 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEMIFSGRAKEE 180
 Db 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEMIFSGRAKEE 180

 QY 181 IVFRYYHKLRMSVEYSQSGWHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSHLGN 240
 Db 181 IVFRYYHKLRMSVEYSQSGWHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSHLGN 240

 QY 241 LVFKKTVILHVSPEERTLVTPAALRPLVLGNGQLVIIVGIVCATILLPVLILVKKTC 300
 Db 241 LVFKKTVILHVSPEERTLVTPAALRPLVLGNGQLVIIVGIVCATILLPVLILVKKTC 300

 QY 301 GNKSSVNSTVLVNTKTNPEIKPCPFCRCEGKHVYSPILVREVIEEESSEKSEAT 360
 Db 301 GNKSSVNSTVLVNTKTNPEIKPCPFCRCEGKHVYSPILVREVIEEESSEKSEAT 360

 QY 361 YMTMHPWPSPSLRDRNNSLEKSGGGMPTQQA 394
 Db 361 YMTMHPWPSPSLRDRNNSLEKSGGGMPTQQA 394

RESULT 5
 AAU12431

ID AAU12431 standard; protein; 394 AA.
 XX AAU12431;
 AC
 XX 24-OCT-2001 (first entry)
 DT
 XX Human PRO1387 polypeptide sequence.
 DE
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO200140466-A2.
 PN
 XX 07-JUN-2001.
 PD
 XX
 PF 01-DEC-2000; 2000WO-US032678.
 XX
 XX 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 03-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen WB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21503.
 DR
 XX
 XX Isolated , secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,

PT breast, prostate, cervical.
XX Claim 12; Fig 520; 813pp; English.
PS
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
Db 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
QY 61 PGEHAKDEYLVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVICEIRL 120
Db 61 PGEHAKDEYLVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVICEIRL 120
QY 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVKVTEWIFSGRRAKEE 180
Db 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVKVTEWIFSGRRAKEE 180
QY 181 IVFRRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLIMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLIMLQGVRESGGNYTCSIHLGN 240
QY 241 LVFKKTIHLVSPPEPRTLTPAALRPLVLGNQLVITVIGVVCATILLPVLILIVKTC 300
Db 241 LVFKKTIHLVSPPEPRTLTPAALRPLVLGNQLVITVIGVVCATILLPVLILIVKTC 300
QY 301 GNKSSVNSTVLVNTKTNPEIKKPCPFERCEGEKHIYSPIIVREVTEEBEPSKSEAT 360
Db 301 GNKSSVNSTVLVNTKTNPEIKKPCPFERCEGEKHIYSPIIVREVTEEBEPSKSEAT 360
QY 361 YMTWHPVWPSLRSDRNSLEKSGGMPKTOQAF 394
Db 361 YMTWHPVWPSLRSDRNSLEKSGGMPKTOQAF 394

RESULT 6
AAM38860
ID AAM38860 standard; protein; 394 AA.
XX
AC AAM38860;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2005.
XX

KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AAI58016.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.
XX
PS Example 3; SEQ ID NO 2005; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nontropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
Db 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
QY 61 PGEHAKDEYLVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVICEIRL 120
Db 61 PGEHAKDEYLVLYYNSLSPVIGRFQNRVHLMGDIILCNDGSLLLQDVQADQGTVICEIRL 120
QY 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVKVTEWIFSGRRAKEE 180
Db 121 KGESQVFKKAVLVHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVKVTEWIFSGRRAKEE 180
QY 181 IVFRRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLIMLQGVRESGGNYTCSIHLGN 240
Db 181 IVFRRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLIMLQGVRESGGNYTCSIHLGN 240

QY 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNQIIVIGIVCATILLPVLILIVKTC 300
 DB 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNQIIVIGIVCATILLPVLILIVKTC 300
 QY 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 DB 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF 394
 DB 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF 394

RESULT 7
 AAB65287
 ID AAB65287 standard; protein; 394 AA.
 AC AAB65287;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1387 (UNQ722) protein sequence SEQ ID NO:422.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
 KW cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 FN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 DF 30-MAR-2000; 2000WO-US008439.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 28-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US000365.
 PR 18-FEB-2000; 2000WO-US000431.
 PR 22-FEB-2000; 2000WO-US000414.
 PR 24-FEB-2000; 2000WO-US0004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kijavlin IU, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WFI; 2001-032160/04.
 DR N-PSDB; AAF44256.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target bioactive

PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX Claim 12; Fig 304; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 394 AA;
 Query Match 100.0%; Score 2067; DB 4; Length 394;
 Best Local Similarity 100.0%; Pred. No. 5.1e-188;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 DB 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTIVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
 QY 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGTVCIRL 120
 DB 61 PGEHAKDEYVLYYNSLVPIGRFQNRVHLMGDIICNDGSLLLQDVQADQGTVCIRL 120
 QY 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWEIFSGRRAKEE 180
 DB 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVWEIFSGRRAKEE 180
 QY 181 IVFYYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCSIHLGN 240
 DB 181 IVFYYHKLMSVEYSQSGHGFQNRVNLVGDIFRNDGSIIMLGVRSDGGNYTCSIHLGN 240
 QY 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNQIIVIGIVCATILLPVLILIVKTC 300
 DB 241 LVFKKTIIVLHVSPEEPTLVTPAALRPLVLGNQIIVIGIVCATILLPVLILIVKTC 300
 QY 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 DB 301 GNKSSVNSTVLVKNTKTNPEIKPKCHFERCEGEKHIYSPIIVREVIEEPEPEKSEAT 360
 QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF 394
 DB 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTKQAF 394

RESULT 8
 AAU83689
 ID AAU83689 standard; protein; 394 AA.
 XX
 AC AAU83689;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 196.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 FN WO200208288-A2.

XX	31-JAN-2002.
PD	
PF	
XX	
XX	29-JUN-2001; 2001WO-US021066.
XX	
XX	20-JUL-2000; 2000US-0219556P.
PR	
PR	25-JUL-2000; 2000US-0220585P.
PR	25-JUL-2000; 2000US-0220603P.
PR	25-JUL-2000; 2000US-0220607P.
PR	25-JUL-2000; 2000US-0220624P.
PR	25-JUL-2000; 2000US-0220638P.
PR	25-JUL-2000; 2000US-0220664P.
PR	25-JUL-2000; 2000US-0220666P.
PR	26-JUL-2000; 2000US-0220893P.
PR	28-JUL-2000; 2000WO-US020710.
PR	01-AUG-2000; 2000US-0222425P.
PR	22-AUG-2000; 2000US-0227133P.
PR	23-AUG-2000; 2000WO-US023522.
PR	24-AUG-2000; 2000WO-US023328.
PR	10-NOV-2000; 2000WO-US030873.
PR	28-NOV-2000; 2000US-0253646P.
PR	01-DEC-2000; 2000WO-US032678.
PR	20-DEC-2000; 2000US-00747259.
PR	20-DEC-2000; 2000WO-US034956.
PR	28-FEB-2001; 2001WO-US006520.
PR	01-MAR-2001; 2001WO-US006666.
PR	22-MAR-2001; 2001US-00816744.
PR	10-MAY-2001; 2001US-00854208.
PR	10-MAY-2001; 2001US-00854280.
PR	25-MAY-2001; 2001WO-US017092.
XX	
XX	(GETH) GENENTECH INC.
PA	
XX	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI	N-PSDB; ABK33633.
DR	WPI; 2002-172001/22.
DR	
XX	One hundred and twenty two nucleic acids encoding PRO polypeptides.
PT	Useful for treating a PRO related disorder and for diagnosing tumors such
PT	as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT	or liver tumor.
XX	
XX	Claim 11; Fig 196; 359pp; English.
PS	
XX	The invention relates to one hundred and twenty two nucleic acids
CC	encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC	encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC	agonists and antagonists are useful for treating a PRO related disorder.
CC	The PRO polypeptides are useful for diagnosing tumours, especially lung
CC	cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC	liver tumour. The PRO polypeptides are useful for stimulating the
CC	proliferation of, or gene expression, in pericyte cells, for stimulating
CC	the proliferation or differentiation of chondrocyte cells, for
CC	stimulating the release of tumour necrosis factor-alpha from human blood,
CC	for stimulating or inhibiting the proliferation of normal human dermal
CC	fibroblast cells. The PRO polypeptide may also be used as molecular
CC	weight markers and for tissue typing. The PRO nucleic acids have
CC	applications in molecular biology, including use as hybridisation probes,
CC	and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC	protein sequences of the invention
XX	
SQ	Sequence 394 AA;
	Query Match 100.0%; Score 2067; DB 5; Length 394;
	Best Local Similarity 100.0%; Pred. No. 5.1e-188;
	Matches 394; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MFCLPLILLPVLLDYSLGLNDLNVSPPELTIVHGDSALMGCVFQSTEDKCIFKDWTLS 60
Db	1 MFCLPLILLPVLLDYSLGLNDLNVSPPELTIVHGDSALMGCVFQSTEDKCIFKDWTLS 60

```

PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88188.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 234; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cycostatic,
CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The PRO polynucleotides have applications in molecular biology,
CC including use as hybridisation probes, and in chromosome and gene
CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC exemplification of the present invention
XX
SQ Sequence 394 AA;
Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKILPVLDDYSLGDLNLSVPELTVHVGDSALMGCVFQSTEDKCFKIDWTL 60
Db 1 MFCPLKILPVLDDYSLGDLNLSVPELTVHVGDSALMGCVFQSTEDKCFKIDWTL 60
QY 61 PGHAKDEYLYYNSLVPIGHFQNRVHLMGDLICNDGSLILLQDVQADQGYICEIRL 120
Db 61 PGHAKDEYLYYNSLVPIGHFQNRVHLMGDLICNDGSLILLQDVQADQGYICEIRL 120
QY 121 KGSQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTVKVEIFSGRRAKEE 180
Db 121 KGSQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTVKVEIFSGRRAKEE 180
QY 181 IVFRRYHKLMSVEYSQSGWGHFQNRVNLVGDIFRNDGSI MLQGVRESDDGNYTCISHLGN 240
Db 181 IVFRRYHKLMSVEYSQSGWGHFQNRVNLVGDIFRNDGSI MLQGVRESDDGNYTCISHLGN 240
QY 241 LVFKKTVLHVSPEEPTLTVPAALRELIVLGGNQLVIIVGIVCATILLPVLILVKKTC 300
Db 241 LVFKKTVLHVSPEEPTLTVPAALRELIVLGGNQLVIIVGIVCATILLPVLILVKKTC 300
QY 301 GNKSVNNTVLVKNTKTNPEIKPCPFCEGEKHIYSPILVREVIEEPESEKSEAT 360
Db 301 GNKSVNNTVLVKNTKTNPEIKPCPFCEGEKHIYSPILVREVIEEPESEKSEAT 360
Db 301 GNKSVNNTVLVKNTKTNPEIKPCPFCEGEKHIYSPILVREVIEEPESEKSEAT 360
QY 361 YMTMHPVWPSLSDRNNLSLEKXSGGMPKTQQAF 394
Db 361 YMTMHPVWPSLSDRNNLSLEKXSGGMPKTQQAF 394
Db 361 YMTMHPVWPSLSDRNNLSLEKXSGGMPKTQQAF 394
RESULT 10
ABB95539
ID ABB95539 standard; protein; 394 AA.
XX
XX ABB95539;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human angiogenesis related protein PRO1387 SEQ ID NO: 234.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cycostatic; antiangiogenic; hypotensive; vulnary;
KW antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX
XX 09-JUL-2001; 2001WO-US021735.
XX
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 22-JAN-2001; 2001US-00767609.
XX 28-FEB-2001; 2001US-00796498.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 09-MAR-2001; 2001US-00802706.
XX 14-MAR-2001; 2001US-00808689.
XX 22-MAR-2001; 2001US-00816744.
XX 05-APR-2001; 2001US-00828366.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866028.
XX 25-MAY-2001; 2001US-00866034.
XX 25-MAY-2001; 2001WO-US017092.
XX 30-MAY-2001; 2001US-00870574.
XX 30-MAY-2001; 2001WO-US017443.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX
XX (GETH ) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERR) FERRARA N.
PA (GERB) GERBER H.
PA (GERR) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.

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PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95677.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 234; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
XX Sequence 394 AA;
XX
Query Match 100.0%; Score 2067; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
DB 1 MFCPLKLLPVLDDYSLGLNDLNVSPPELVHVGDSALMGCVFQSTEDKCFKIDWTLS 60
QY 61 PGEHAKDEVLYYYNSLSVPIGRFQNRVHLMGDIICNDGSLLLQDVQEQDQGYVICIRL 120
DB 61 PGEHAKDEVLYYYNSLSVPIGRFQNRVHLMGDIICNDGSLLLQDVQEQDQGYVICIRL 120
QY 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMCCVFQSTEVKHVTVKVEWIFSGRRAKEE 180
DB 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMCCVFQSTEVKHVTVKVEWIFSGRRAKEE 180
QY 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHIGN 240
DB 181 IVFRYHKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSLMLQGVRESGGNYTCSIHIGN 240
QY 241 LVFKKTIHLVHVSPEEPRTLTPAALRPLVGGNQLVIIVGIVCATILLLPVLILIVKTC 300
DB 241 LVFKKTIHLVHVSPEEPRTLTPAALRPLVGGNQLVIIVGIVCATILLLPVLILIVKTC 300
QY 301 GNKSSVNSTVLVKNKTNPKEIKKPCHEKPCHEKHIYSPILIVREIREEPSEKSEAT 360
DB 301 GNKSSVNSTVLVKNKTNPKEIKKPCHEKPCHEKHIYSPILIVREIREEPSEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQAF 394
DB 361 YMTMHPVWPSLRSDRNNLSLEKSGGGMPTQQAF 394
XX
RESULT 11
ABUS8102
ID ABUS8102 standard; protein; 394 AA.
XX
AC ABUS8102;
XX
```

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DT 14-APR-2003 (first entry)
XX Human PRO polypeptide #134.
DE
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
XX US2003027163-A1.
XX
XX 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087559P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 23-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
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Db 241 LVFKKTVLVHVSPEEPTLVTPAALPLVLGGNQLVIVGIVCATILLPLVLILVKKTC 300
Qy 301 GNKSSVNSTVLVKTKTNPIKPKCHPERCEBGEKHIYSPIIVREVIEEPEKSEAT 360
Db 301 GNKSSVNSTVLVKTKTNPIKPKCHPERCEBGEKHIYSPIIVREVIEEPEKSEAT 360
Qy 361 YMTWHPVWPSLRSRDNNSLEKSGGMPKTOQAF 394
Db 361 YMTWHPVWPSLRSRDNNSLEKSGGMPKTOQAF 394

RESULT 12
ABUS9180
ID ABUS9180 standard; protein; 394 AA.
XX AC ABUS9180;
XX DT 28-APR-2003 (first entry)
XX DE Novel human secreted or transmembrane protein PRO1387.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX OS Homo sapiens.
XX PN US2002132252-A1.
XX PD 19-SEP-2002.
XX PE 14-NOV-2001; 2001US-00990442.
XX PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 03-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 09-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.

10-JUN-1998; 98US-0088826P.
11-JUN-1998; 98US-0088858P.
11-JUN-1998; 98US-0088861P.
11-JUN-1998; 98US-0088876P.
12-JUN-1998; 98US-0089105P.
16-JUN-1998; 98US-0089440P.
16-JUN-1998; 98US-0089512P.
16-JUN-1998; 98US-0089514P.
17-JUN-1998; 98US-0089532P.
17-JUN-1998; 98US-0089538P.
17-JUN-1998; 98US-0089598P.
17-JUN-1998; 98US-0089599P.
17-JUN-1998; 98US-0089600P.
17-JUN-1998; 98US-0089653P.
18-JUN-1998; 98US-0089801P.
18-JUN-1998; 98US-0089907P.
18-JUN-1998; 98US-0089908P.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98WO-US019437.
07-OCT-1998; 98WO-US021141.
01-DEC-1998; 98WO-US025108.
05-JAN-1999; 99WO-US000106.
08-MAR-1999; 99WO-US005028.
02-JUN-1999; 99WO-US012252.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
01-DEC-1999; 99WO-US028634.
16-DEC-1999; 99WO-US030095.
20-DEC-1999; 99WO-US030911.
06-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
28-AUG-2001; 2001US-00941992.
XX (GETH) GENENTECH INC.
XX PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Geber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2003-247083/24.
DR N-FSDB; AEX80392.
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1184, PRO1346
PT

PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
XX treatments.
PS Claim 12; Fig 304; 649pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
Db 1 MFCPLKLLPVLIDYSLGNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIKIDWTLS 60
QY 61 PGEHAKDEYVLYYSNLVSPIGRPNRVLHMGDILNDGSLLLQDVQADQGTVCIRL 120
Db 61 PGEHAKDEYVLYYSNLVSPIGRPNRVLHMGDILNDGSLLLQDVQADQGTVCIRL 120
QY 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
Db 121 KGESQVFKKAVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEE 180
QY 181 IVFYYHKLMSVEYSQSGWHQFQNRVNLVGDIFRNDGSIIMLQGVRESDDGNYTCSIHLGN 240
Db 181 IVFYYHKLMSVEYSQSGWHQFQNRVNLVGDIFRNDGSIIMLQGVRESDDGNYTCSIHLGN 240
QY 241 LVFKKTVLHVSPEERTLVTAAALRPLVIGNQLVIVGIVCATILLPVLILVKKTC 300
Db 241 LVFKKTVLHVSPEERTLVTAAALRPLVIGNQLVIVGIVCATILLPVLILVKKTC 300
QY 301 GNKSSVNSTVLVNTKTNPEIKKPCPCRCGEKHIIYSPVIREVIEEPEEPESEKSEAT 360
Db 301 GNKSSVNSTVLVNTKTNPEIKKPCPCRCGEKHIIYSPVIREVIEEPEEPESEKSEAT 360
QY 361 YMTMHPVWPVSLRDRNNSLEKKGSGGMPKTKQAF 394
Db 361 YMTMHPVWPVSLRDRNNSLEKKGSGGMPKTKQAF 394

RESULT 13
ABU82692

ID ABU82692 standard; protein; 394 AA.
XX AC ABU82692;
XX DT 26-JUN-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO1387.
XX KW Human; PRO; secreted protein; transmembrane protein;
XX KW cardiac insufficiency disorders; angiogenesis; wound healing;
XX KW cancerous tumour; immune response; retinal disorder; sight loss;
XX KW retinitis pigmentosa; age-related macular degeneration; AMD;
XX KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
XX KW Crohn's disease; sports injury; arthritis.
XX OS Homo sapiens.
XX PN US2003032023-A1.
XX PD 13-FEB-2003.
XX PF 14-NOV-2001; 2001US-00990711.
XX PR 16-JUN-1997; 97US-0049787P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 05-NOV-1997; 97WO-US020069.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 24-NOV-1997; 97US-0066770P.
XX PR 25-FEB-1998; 98US-0075945P.
XX PR 20-MAR-1998; 98US-0078910P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 07-MAY-1998; 98US-0084600P.
XX PR 02-JUN-1998; 98US-0087106P.
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 03-JUN-1998; 98US-0087759P.
XX PR 04-JUN-1998; 98US-0088021P.
XX PR 04-JUN-1998; 98US-0088025P.
XX PR 04-JUN-1998; 98US-0088026P.
XX PR 04-JUN-1998; 98US-0088028P.
XX PR 04-JUN-1998; 98US-0088029P.
XX PR 04-JUN-1998; 98US-0088030P.
XX PR 04-JUN-1998; 98US-0088033P.
XX PR 05-JUN-1998; 98US-0088326P.
XX PR 05-JUN-1998; 98US-0088167P.
XX PR 05-JUN-1998; 98US-0088202P.
XX PR 05-JUN-1998; 98US-0088212P.
XX PR 05-JUN-1998; 98US-0088217P.
XX PR 09-JUN-1998; 98US-0088655P.
XX PR 10-JUN-1998; 98US-0088734P.
XX PR 10-JUN-1998; 98US-0088738P.
XX PR 10-JUN-1998; 98US-0088742P.
XX PR 10-JUN-1998; 98US-0088810P.
XX PR 10-JUN-1998; 98US-0088824P.
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XX PR 11-JUN-1998; 98US-0088858P.
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XX PR 16-JUN-1998; 98US-0089440P.
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XX PR 17-JUN-1998; 98US-0089598P.
XX PR 17-JUN-1998; 98US-0089599P.
XX PR 17-JUN-1998; 98US-0089600P.
XX PR 17-JUN-1998; 98US-0089653P.
XX PR 18-JUN-1998; 98US-0089801P.
XX PR 18-JUN-1998; 98US-0089907P.
XX PR 18-JUN-1998; 98US-0089908P.

PR	19-JUN-1998;	98US-0089947P.	PR	26-AUG-1998;	98US-0097954P.
PR	19-JUN-1998;	98US-0089948P.	PR	26-AUG-1998;	98US-0097955P.
PR	19-JUN-1998;	98US-0089952P.	PR	26-AUG-1998;	98US-0097971P.
PR	22-JUN-1998;	98US-0090246P.	PR	26-AUG-1998;	98US-0097974P.
PR	22-JUN-1998;	98US-0090252P.	PR	26-AUG-1998;	98US-0097978P.
PR	22-JUN-1998;	98US-0090254P.	PR	26-AUG-1998;	98US-0097979P.
PR	23-JUN-1998;	98US-0090349P.	PR	26-AUG-1998;	98US-0097986P.
PR	23-JUN-1998;	98US-0090355P.	PR	26-AUG-1998;	98US-0098014P.
PR	24-JUN-1998;	98US-0090429P.	PR	31-AUG-1998;	98US-0098525P.
PR	24-JUN-1998;	98US-0090431P.	PR	16-SEP-1998;	98US-0100634P.
PR	24-JUN-1998;	98US-0090435P.	PR	16-SEP-1998;	98WO-US019330.
PR	24-JUN-1998;	98US-0090445P.	PR	17-SEP-1998;	98US-0100858P.
PR	24-JUN-1998;	98US-0090447P.	PR	17-SEP-1998;	98WO-US019437.
PR	24-JUN-1998;	98US-0090472P.	PR	01-OCT-1998;	98WO-US021141.
PR	24-JUN-1998;	98US-0090535P.	PR	01-DEC-1998;	98WO-US025108.
PR	24-JUN-1998;	98US-0090540P.	PR	22-DEC-1998;	98US-0113296P.
PR	24-JUN-1998;	98US-0090542P.	PR	05-JAN-1999;	99WO-US000106.
PR	24-JUN-1998;	98US-0090557P.	PR	08-MAR-1999;	99WO-US0005028.
PR	25-JUN-1998;	98US-0090676P.	PR	12-MAR-1999;	99US-0123957P.
PR	25-JUN-1998;	98US-0090678P.	PR	02-JUN-1999;	99WO-US012252.
PR	25-JUN-1998;	98US-0090690P.	PR	23-JUN-1999;	99US-0141037P.
PR	25-JUN-1998;	98US-0090694P.	PR	07-JUL-1999;	99US-0143048P.
PR	25-JUN-1998;	98US-0090695P.	PR	20-JUL-1999;	99US-0144758P.
PR	25-JUN-1998;	98US-0090696P.	PR	26-JUL-1999;	99US-0145698P.
PR	26-JUN-1998;	98US-0090862P.	PR	28-JUL-1999;	99US-0146222P.
PR	26-JUN-1998;	98US-0090863P.	PR	17-AUG-1999;	99US-0149396P.
PR	01-JUL-1998;	98US-0091360P.	PR	15-SEP-1999;	99WO-US021090.
PR	01-JUL-1998;	98US-0091544P.	PR	15-SEP-1999;	99WO-US0211547.
PR	02-JUL-1998;	98US-0091478P.	PR	08-OCT-1999;	99US-0158663P.
PR	02-JUL-1998;	98US-0091519P.	PR	30-NOV-1999;	99WO-US028313.
PR	02-JUL-1998;	98US-0091626P.	PR	01-DEC-1999;	99WO-US028301.
PR	02-JUL-1998;	98US-0091628P.	PR	01-DEC-1999;	99WO-US028634.
PR	02-JUL-1998;	98US-0091633P.	PR	16-DEC-1999;	99WO-US030095.
PR	02-JUL-1998;	98US-0091646P.	PR	20-DEC-1999;	99WO-US030911.
PR	02-JUL-1998;	98US-0091673P.	PR	05-JAN-2000;	2000WO-US000219.
PR	07-JUL-1998;	98US-0091987P.	PR	06-JAN-2000;	2000WO-US000376.
PR	07-JUL-1998;	98US-0091988P.	PR	11-FEB-2000;	2000WO-US003565.
PR	09-JUL-1998;	98US-0092182P.	PR	18-FEB-2000;	2000WO-US004341.
PR	10-JUL-1998;	98US-0092472P.	PR	22-FEB-2000;	2000WO-US004414.
PR	20-JUL-1998;	98US-0093339P.	PR	24-FEB-2000;	2000WO-US004914.
PR	30-JUL-1998;	98US-0094651P.	PR	24-FEB-2000;	2000WO-US005004.
PR	04-AUG-1998;	98US-0095282P.	PR	02-MAR-2000;	2000WO-US005841.
PR	04-AUG-1998;	98US-0095285P.	PR	10-MAR-2000;	2000WO-US006319.
PR	04-AUG-1998;	98US-0095301P.	PR	15-MAR-2000;	2000WO-US006884.
PR	04-AUG-1998;	98US-0095302P.	PR	20-MAR-2000;	2000WO-US007377.
PR	04-AUG-1998;	98US-0095318P.	PR	30-MAR-2000;	2000WO-US008439.
PR	04-AUG-1998;	98US-0095321P.	PR	15-MAY-2000;	2000WO-US013358.
PR	04-AUG-1998;	98US-0095325P.	PR	17-MAY-2000;	2000WO-US013705.
PR	10-AUG-1998;	98US-0095916P.	PR	22-MAY-2000;	2000WO-US014042.
PR	10-AUG-1998;	98US-0095929P.	PR	30-MAY-2000;	2000WO-US014941.
PR	11-AUG-1998;	98US-0096012P.	PR	02-JUN-2000;	2000WO-US015264.
PR	11-AUG-1998;	98US-0096143P.	PR	23-JUN-2000;	2000US-0213637P.
PR	11-AUG-1998;	98US-0096146P.	PR	28-JUL-2000;	2000WO-US020710.
PR	17-AUG-1998;	98US-0096757P.	PR	11-AUG-2000;	2000WO-US022031.
PR	17-AUG-1998;	98US-0096766P.	Query Match 100.0%; Score 2067; DB 6; Length 394;		
PR	17-AUG-1998;	98US-0096768P.	Best Local Similarity 100.0%; Pred. No. 5.1e-188;		
PR	17-AUG-1998;	98US-0096773P.	Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
PR	17-AUG-1998;	98US-0096791P.			
PR	17-AUG-1998;	98US-0096867P.	Qy	1	MFCPLKLLLPVLLDYSIGLNDLNVSPPELTVHVHGDLSALMGCVFQSTEDKCIFKIDWTLS 60
PR	17-AUG-1998;	98US-0096891P.	Db	1	MFCPLKLLLPVLLDYSIGLNDLNVSPPELTVHVHGDLSALMGCVFQSTEDKCIFKIDWTLS 60
PR	17-AUG-1998;	98US-0096894P.			
PR	17-AUG-1998;	98US-0096895P.			
PR	17-AUG-1998;	98US-0096897P.	Qy	61	PGEHAKDEYVLYYYNSLVPIGRFQNRVHLMGDI LCNDGSLLLQDVQEADGQTYICEIRL 120
PR	18-AUG-1998;	98US-0096949P.	Db	61	PGEHAKDEYVLYYYNSLVPIGRFQNRVHLMGDI LCNDGSLLLQDVQEADGQTYICEIRL 120
PR	18-AUG-1998;	98US-0096950P.			
PR	18-AUG-1998;	98US-0096959P.	Qy	121	KGESQVFKA VLVHVPPEPKELMVHVGGLIQMCVCFQSTEVKHTKVWEIFSGRRAKEE 180
PR	18-AUG-1998;	98US-0096960P.	Db	121	KGESQVFKA VLVHVPPEPKELMVHVGGLIQMCVCFQSTEVKHTKVWEIFSGRRAKEE 180
PR	18-AUG-1998;	98US-0097022P.			
PR	19-AUG-1998;	98US-0097141P.			
PR	20-AUG-1998;	98US-0097218P.	Qy	181	IVFRIYHKL RMSVEYQS WGHFQNRVNL VGDIFRNDGSI MLOGVRES DGGNYTCSIHUIGN 240
PR	24-AUG-1998;	98US-0097661P.			
PR	26-AUG-1998;	98US-0097952P.			

Db 181 IVFRYYHKLMSVEYSQSGWHGFQNRKVLNVDIFRNDGSGIMLQGVRESGGNYTCSIHLGN 240
QY 241 LVFKKTIIVLHVSPEPPTLVTPAALRPLVLGGNQLVIIVGIVCATITLLPVLLIIVKTC 300
Db 241 LVFKKTIIVLHVSPEPPTLVTPAALRPLVLGGNQLVIIVGIVCATITLLPVLLIIVKTC 300
QY 301 GNKSSVNSTVLVKNTKTNPEIKKPCHFCECEKEKHIYSPILVREVIEEPESEKSEAT 360
Db 301 GNKSSVNSTVLVKNTKTNPEIKKPCHFCECEKEKHIYSPILVREVIEEPESEKSEAT 360
QY 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394
Db 361 YMTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394
RESULT 14
ABO17875
ID ABO17875 standard; protein; 394 AA.
XX AC ABO17875;
XX DT 26-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1387.
XX KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX OS Homo sapiens.
XX PN US2003032156-A1.
XX PD 13-FEB-2003.
XX PF 06-MAY-2002; 2002US-00140474.
XX PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 03-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 28-JUL-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00802706.
PR 22-MAR-2001; 2001US-00808689.
PR 05-APR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PA (GETH) GENENTECH INC.
XX

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD24112.
XX
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 520; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 394 AA;

Query Match 100.0%; Score 2067; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 5,1e-188;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFCPLKLLPVLLDYSLGLNDLNVSPPELTVHVHGLMVGCVFQSTEDKCIKIDWTLS 60
Db 1 MFCPLKLLPVLLDYSLGLNDLNVSPPELTVHVHGLMVGCVFQSTEDKCIKIDWTLS 60

Qy 61 PGEHAKDEYLYYYSNLSVPVIGRFQNRVHLMGDILCNDGSLLLQDVQADQGYTICEIRL 120
Db 61 PGEHAKDEYLYYYSNLSVPVIGRFQNRVHLMGDILCNDGSLLLQDVQADQGYTICEIRL 120

Qy 121 KGESQVFKAVVHLVLPPEPKELMVHVGGLTQMGCVFQSTEVKHVTKVWFVSGRAKEE 180
Db 121 KGESQVFKAVVHLVLPPEPKELMVHVGGLTQMGCVFQSTEVKHVTKVWFVSGRAKEE 180

Qy 181 IVFRYHKLRLMSVEYSQWGHFQNRVNLVGDIFRNDGSGIMLQGVRESGNGYTCIHLGN 240
Db 181 IVFRYHKLRLMSVEYSQWGHFQNRVNLVGDIFRNDGSGIMLQGVRESGNGYTCIHLGN 240

Qy 241 LVFKKTIVLHVSPEEPRTLVTTPAALRPLVLGNGQLVIVGIVCATILLPLVLIVKTC 300
Db 241 LVFKKTIVLHVSPEEPRTLVTTPAALRPLVLGNGQLVIVGIVCATILLPLVLIVKTC 300

Qy 301 GNKSSVNSVLVKNTKTNPEIKKPCHEFCERCEGKHYSPIIVREVEIEEPESEKSEAT 360
Db 301 GNKSSVNSVLVKNTKTNPEIKKPCHEFCERCEGKHYSPIIVREVEIEEPESEKSEAT 360

Qy 361 YNTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394
Db 361 YNTMHPVWPSLRSDRNNLSLEKSGGMPKTOQAF 394

RESULT 15

ABU60611
ID ABU60611 standard; protein; 394 AA.
XX
AC ABU60611;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #170.
XX
KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
XX diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992598.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.

